

Species-level systematics of *Bartsia*
(Orobanchaceae): a multilocus approach with
complete sampling and hundreds of individuals
for a rapid and recent Andean radiation

Simon Uribe-Convers and David C. Tank

University of Idaho

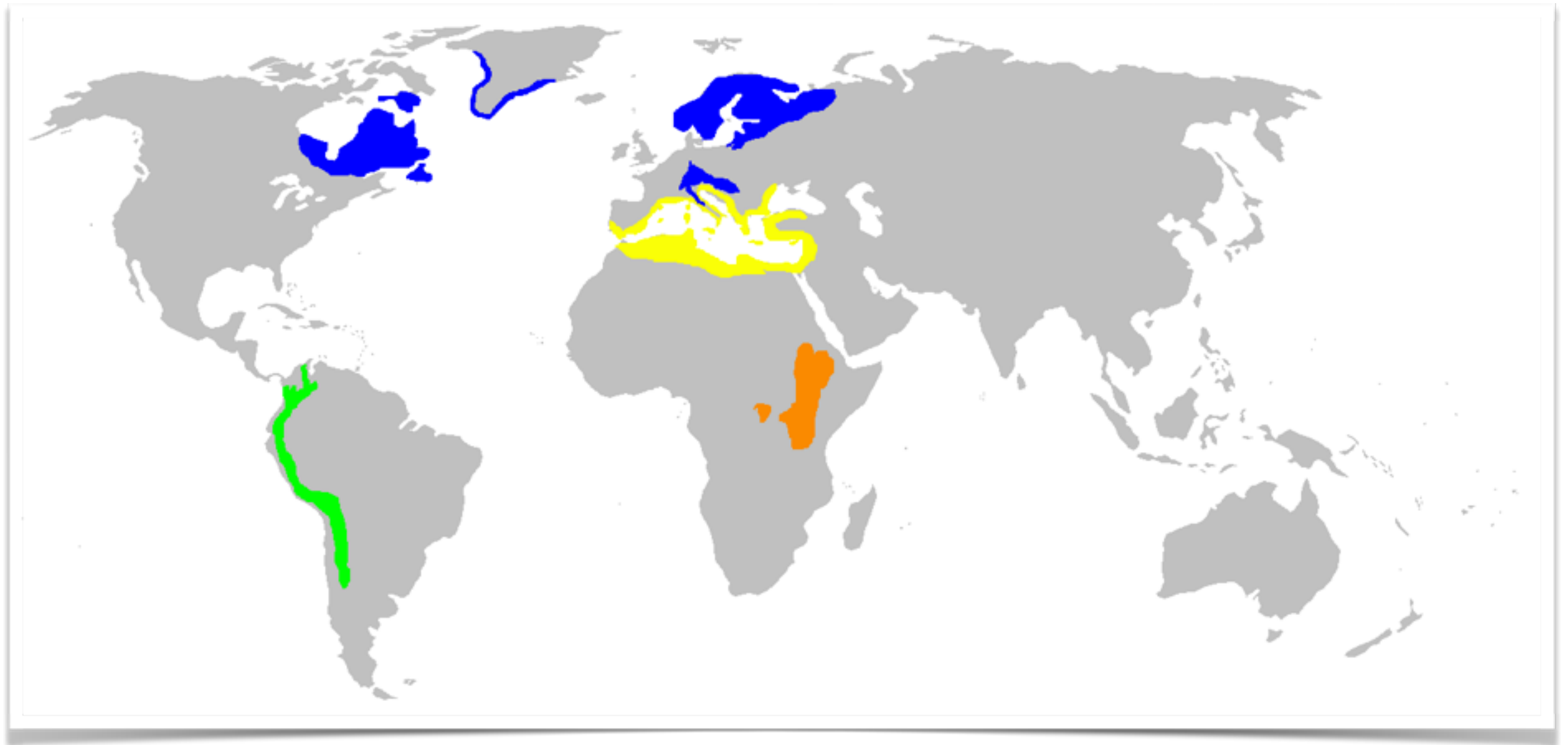
 @uribe_convers

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- Linnaeus
- Herbs and shrubs
- Hemiparasite
- Alpine ecosystems
- ca. 49 species



- 2 species in Africa
 - 1 species in Europe and northeastern North America
 - 1 species in the Mediterranean
 - ca. 45 species in South America
- high levels of sympatry





12 7-1848

Emphrasia holliana Lowe in
Trans. Camb. phil. soc. IV ()
p. 20. - *Emph. Primit. fl. ar. form.*
Madag. (1891) p. 20.

Fixago scordifolia R. & A. in
Flora ed. Bot. Zool. 1832, p. 126

Emphrasia scordifolia Spreng. Nomen
clat. ed. 2^a (1845) p. 189 (nomen)

Odontites holliana Benth. in
Decand. prodr. X (1846) p. 551, n. 9.

HERB. J. GAY.
Presented by Dr. Hooker, February 1868.

Bartia holliana, Benth.
C.B. Clarke
10 Dec. 1903

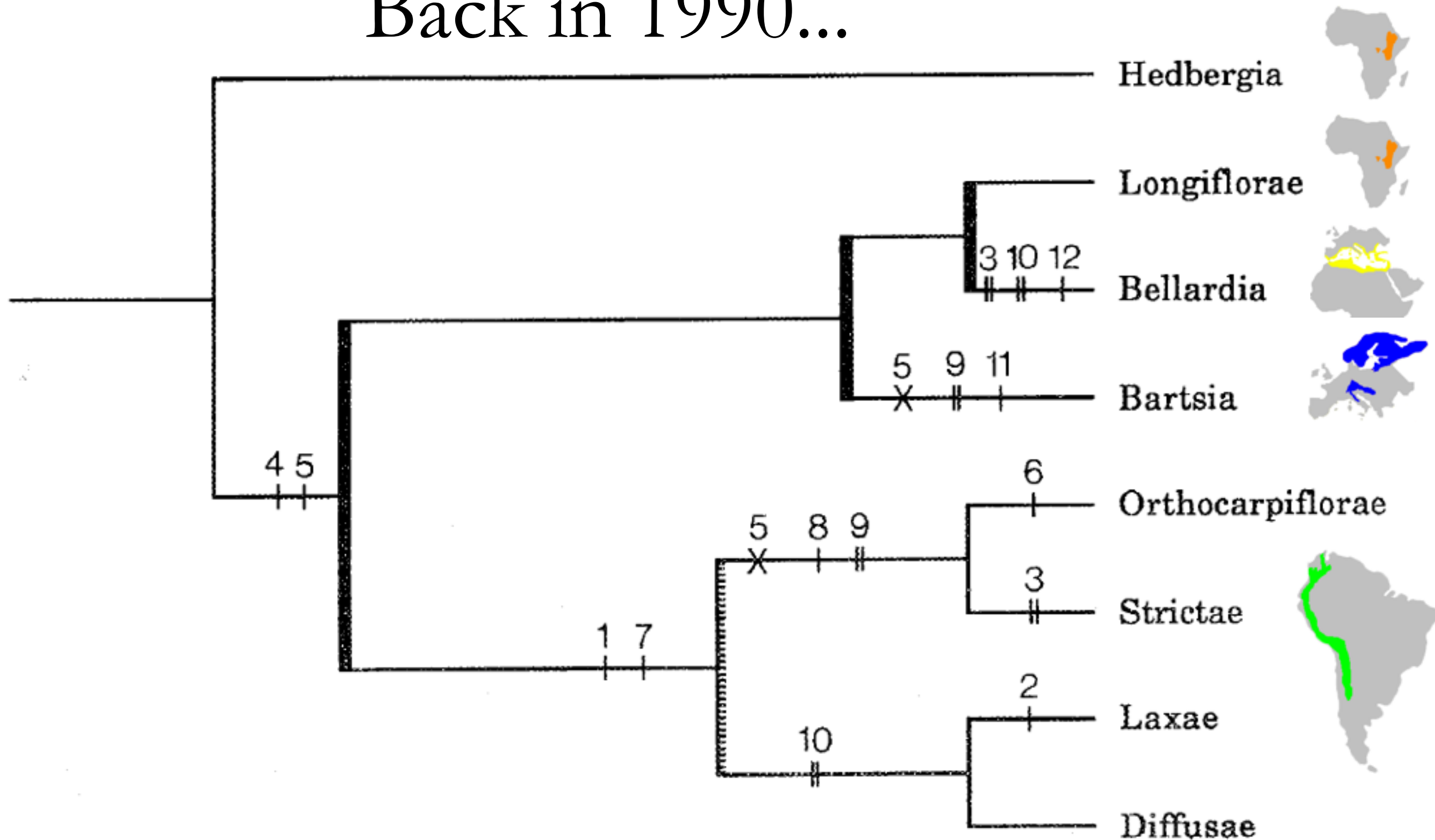
Odontites hollianus (R. Lowe) Benth.
det. M. Bolliger 1992

Emphrasia holliana, Lowe Benth.
Fl. ar. ed. 2^a (1845) p. 189, n. 9.

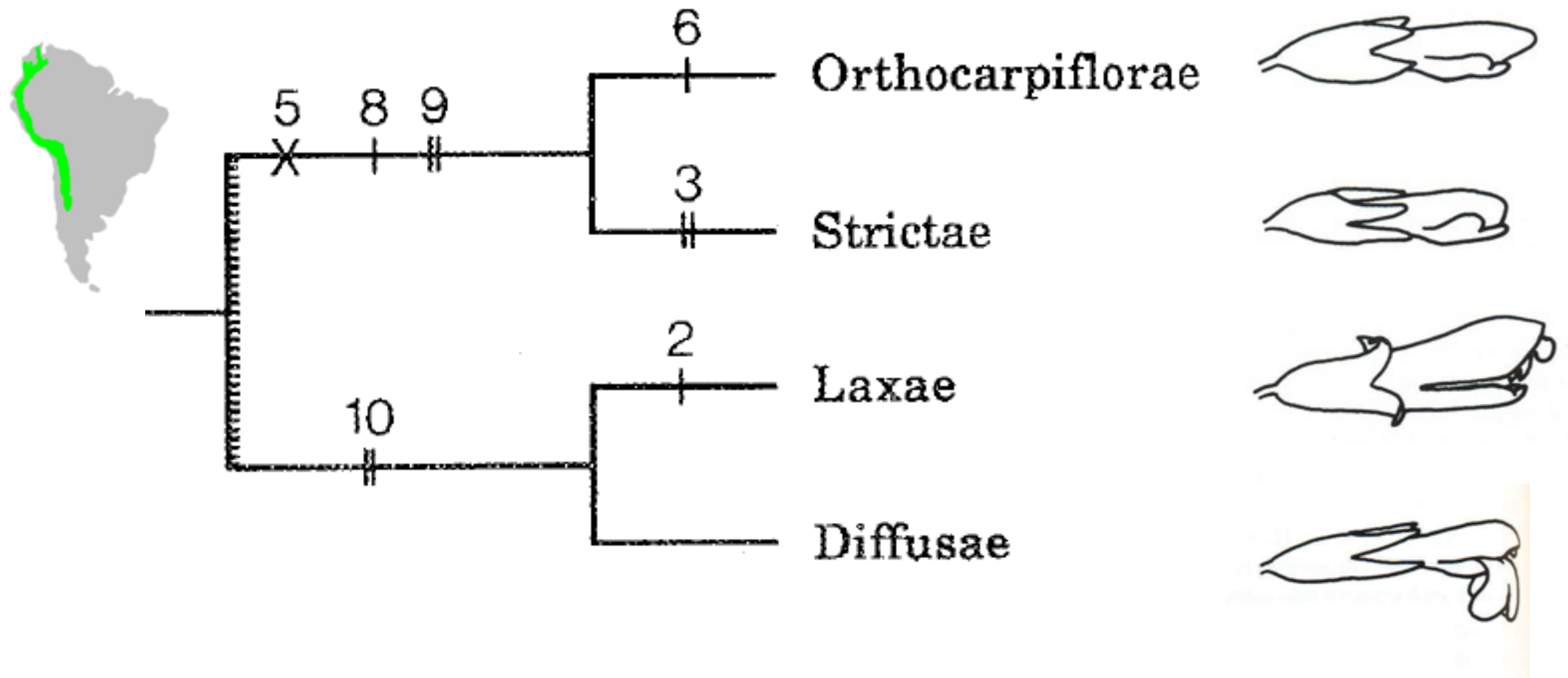
January 1868.
[unclear] (unclear)
[unclear] [unclear]

Rosa flava -

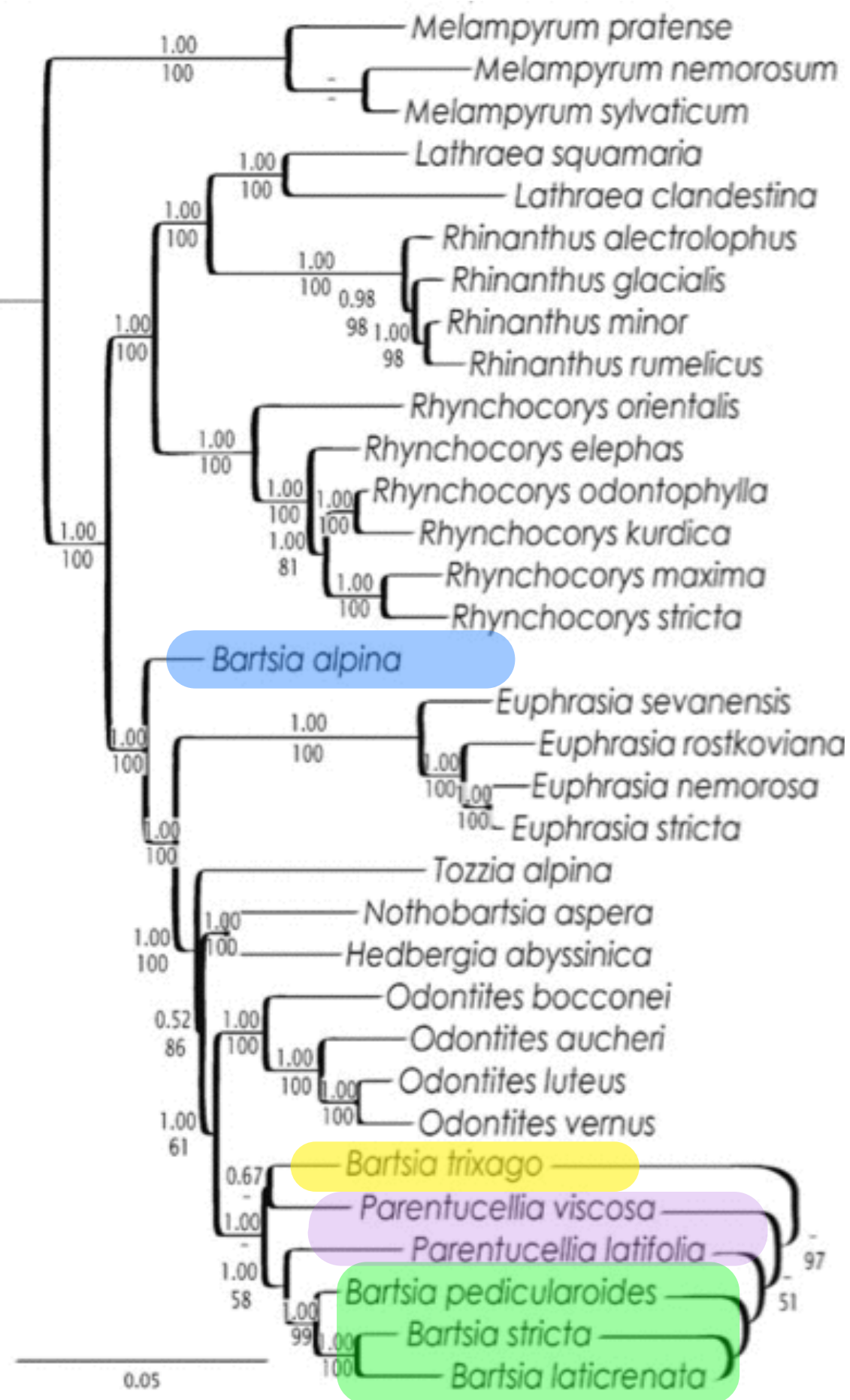
Back in 1990...



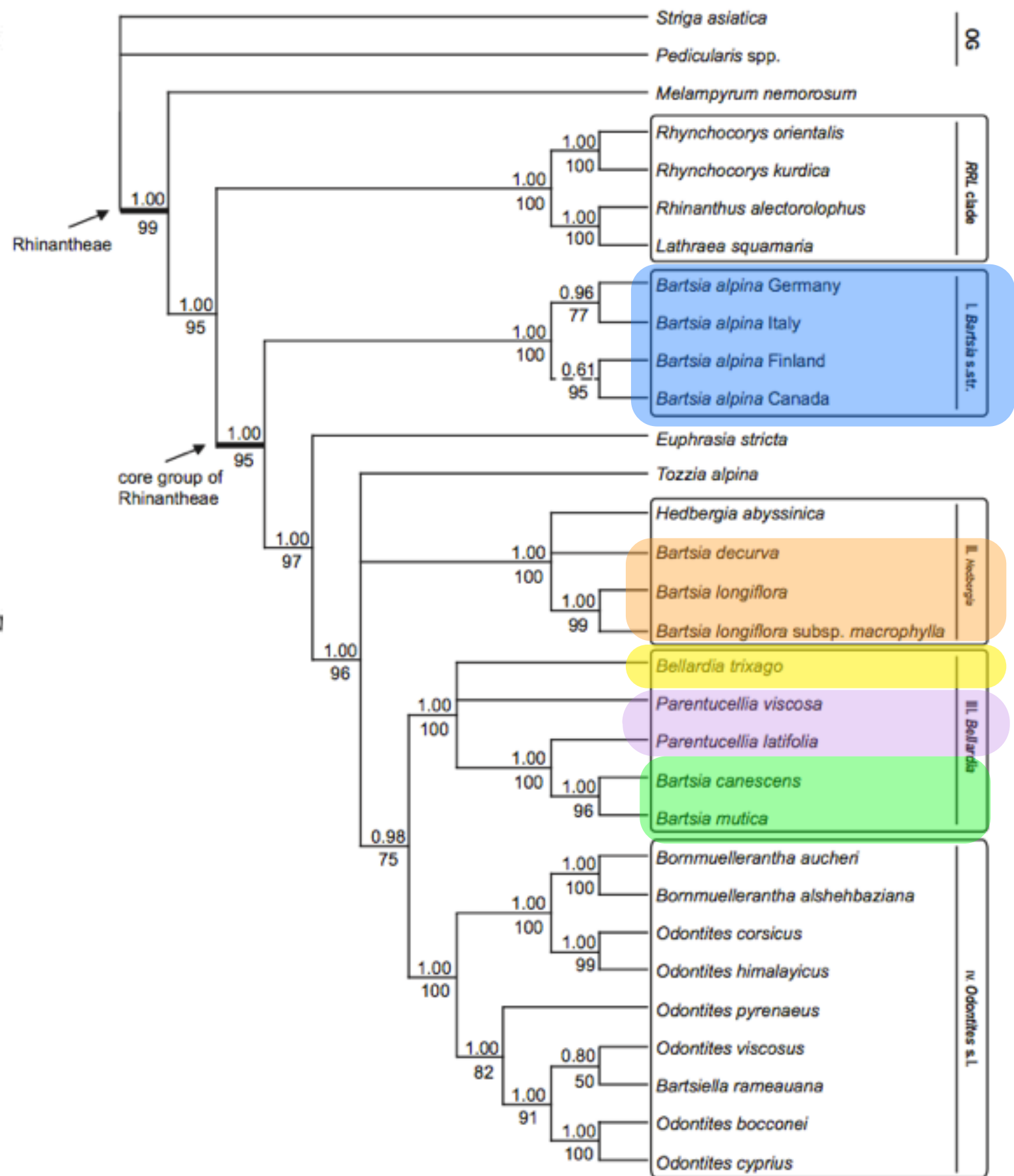
Back in 1990...



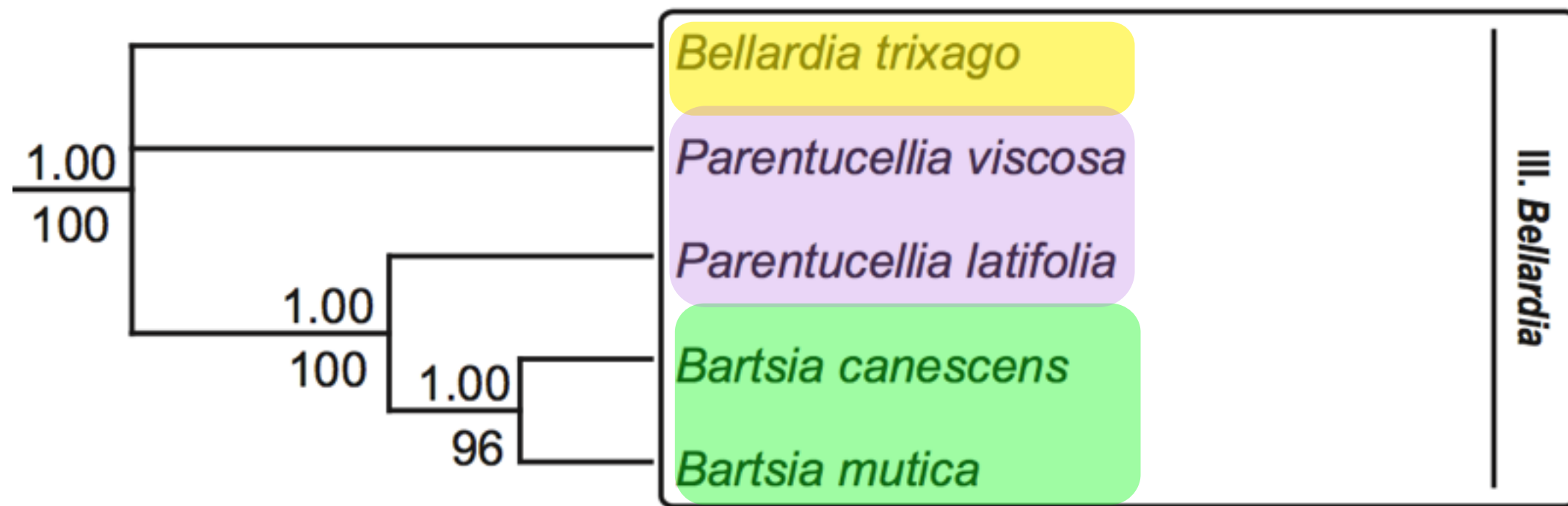




Těšitel et al., 2010



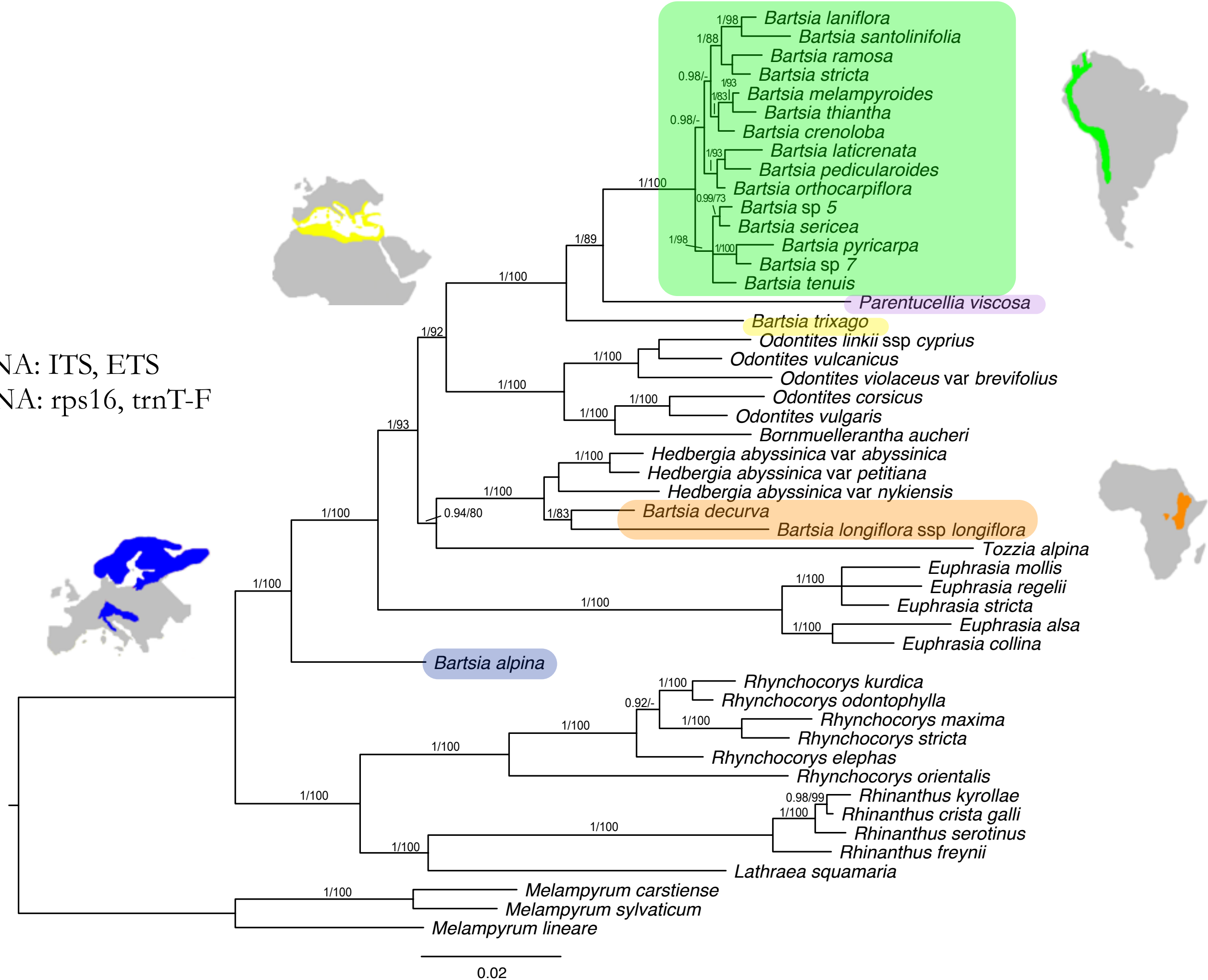
Scheunert et al., 2012

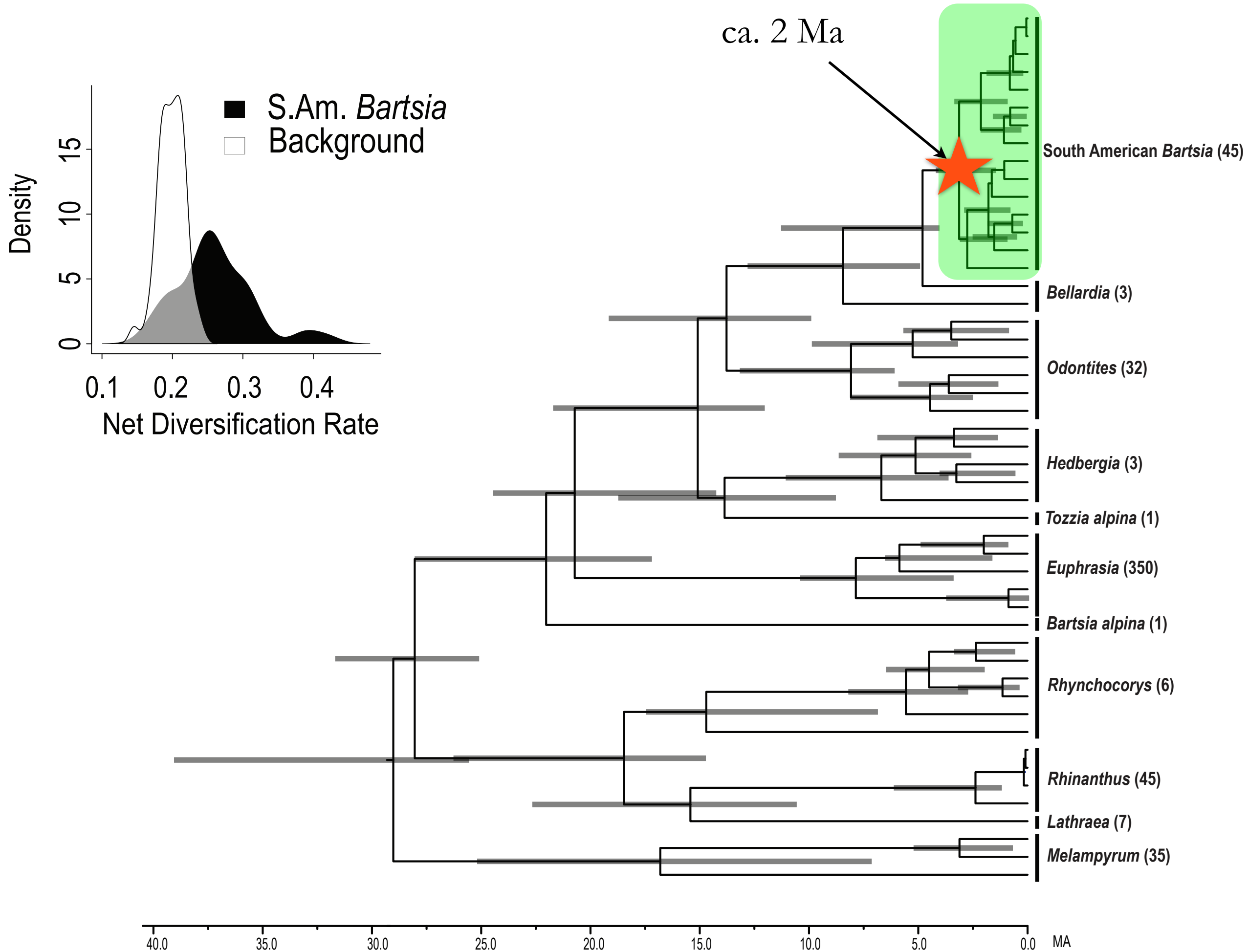


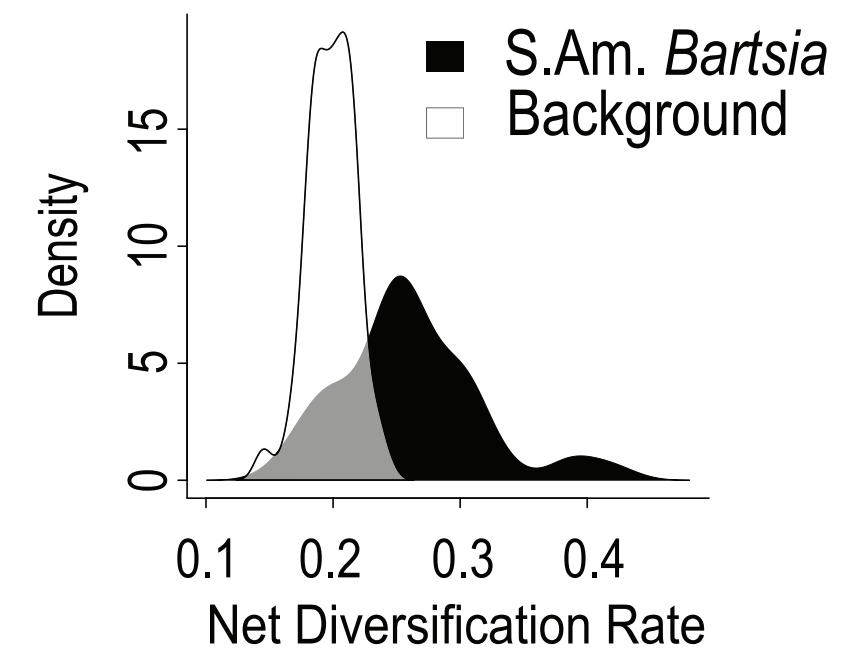
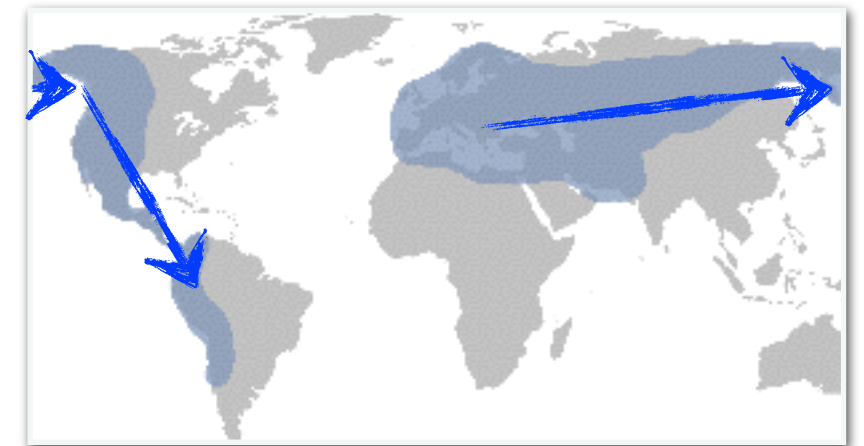
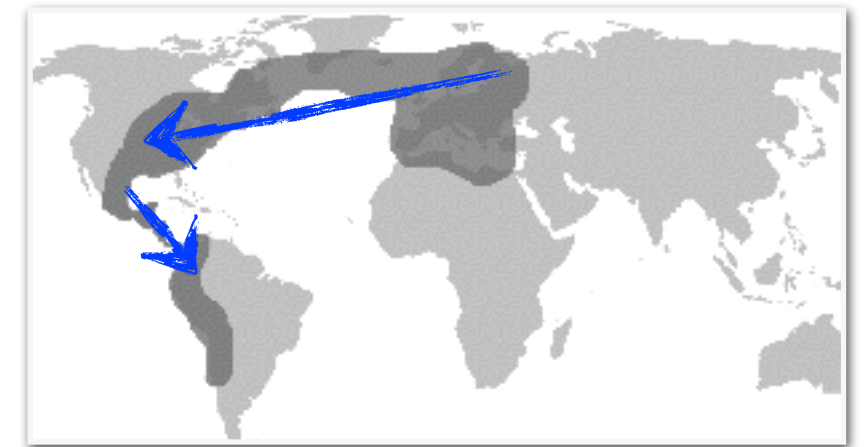
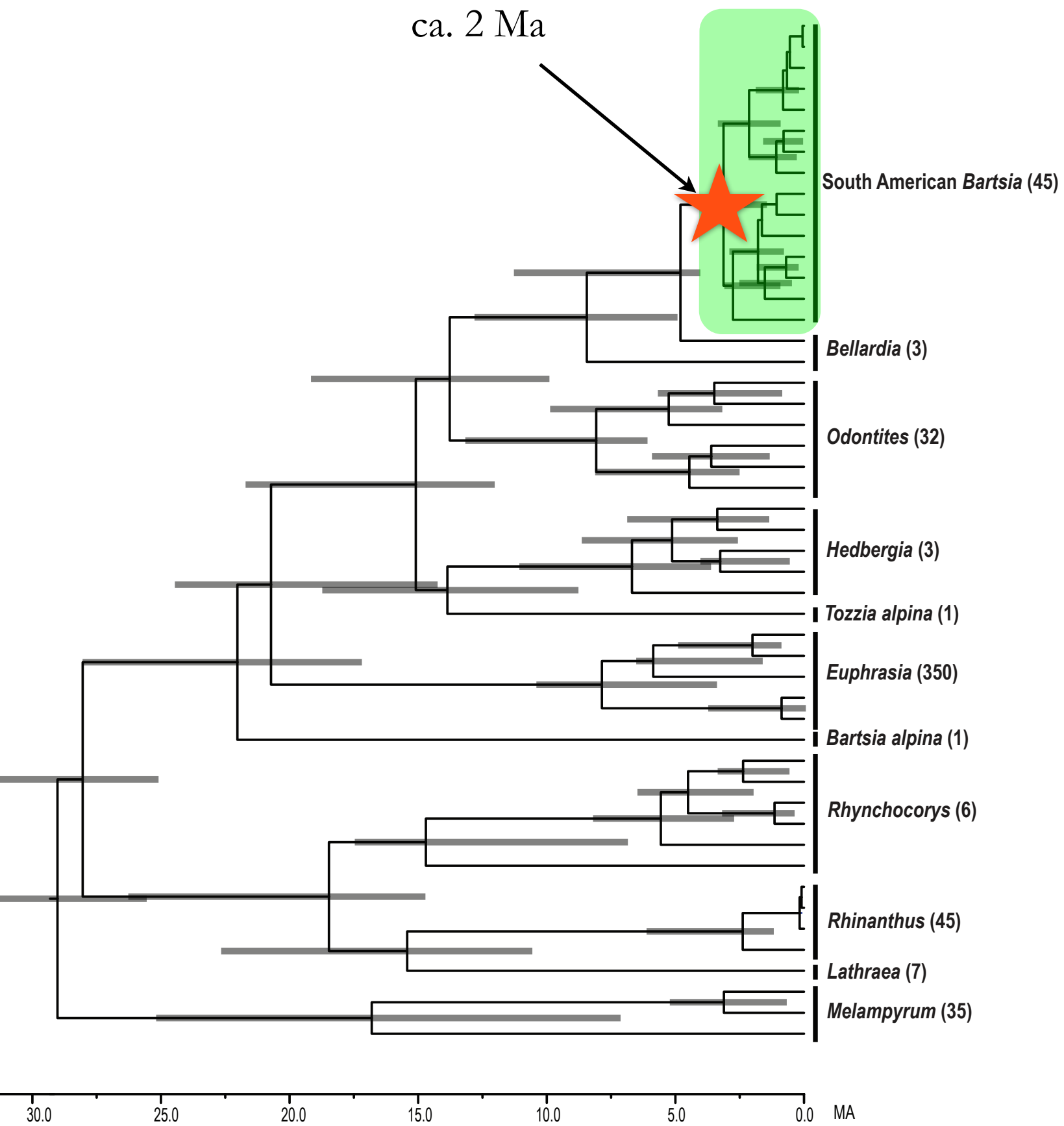
Bellardia All.



nrDNA: ITS, ETS
cpDNA: rps16, trnT-F









Bellardia trixago (L.) All.



Bellardia viscosa
(L.) Fisch. & C.A. Mey



Bellardia latifolia (L.) Cuatrec.

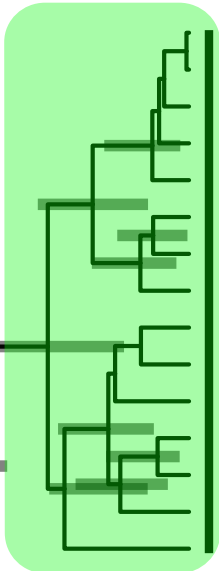


South American *Bartsia*

Bellardia All.



Modified from Scheunert et al., 2012



Bellardia

Bellardia (3)

Odontites (32)

Hedbergia (3)

Tozzia alpina (1)

Euphrasia (350)

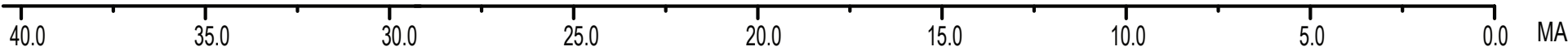
Bartsia alpina (1)

Rhynchocorys (6)

Rhinanthus (45)

Lathraea (7)

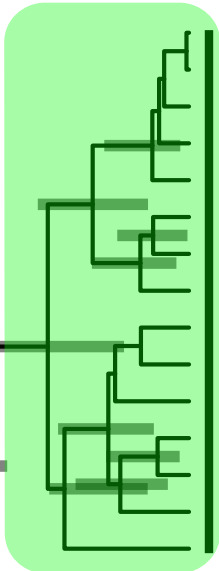
Melampyrum (35)



Bellardia All.



Modified from Scheunert et al., 2012



Neobartsia Uribe-Convers & Tank

Parentucellia latifolia
Pseudoparentucellia viscosa Uribe-Convers & Tank

Bellardia trixago

Odontites (32)

Hedbergia (3)

Tozzia alpina (1)

Euphrasia (350)

Bartsia alpina (1)

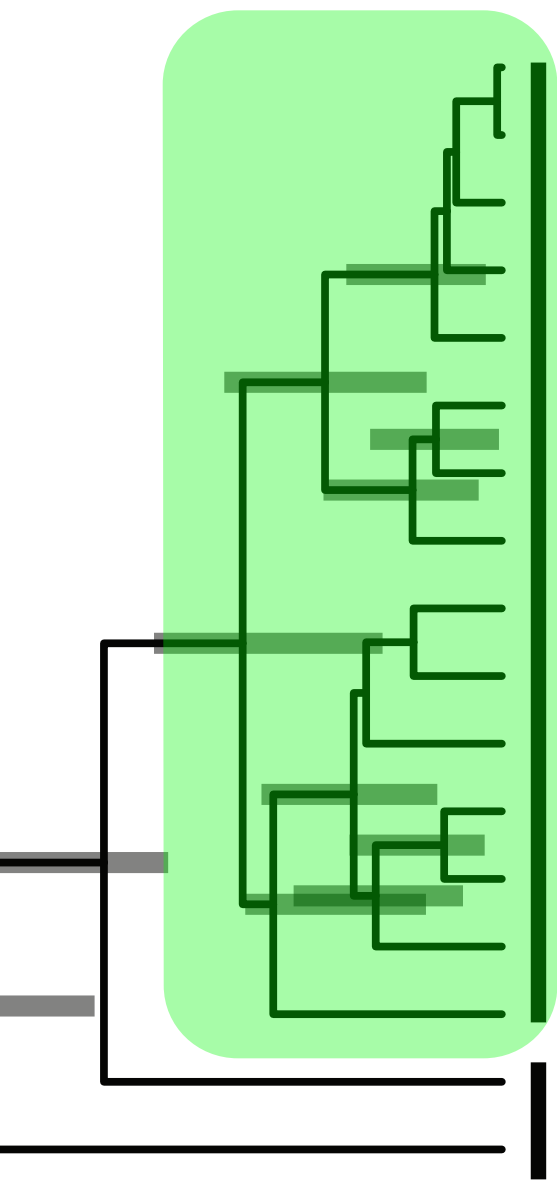
Rhynchocorys (6)

Rhinanthus (45)

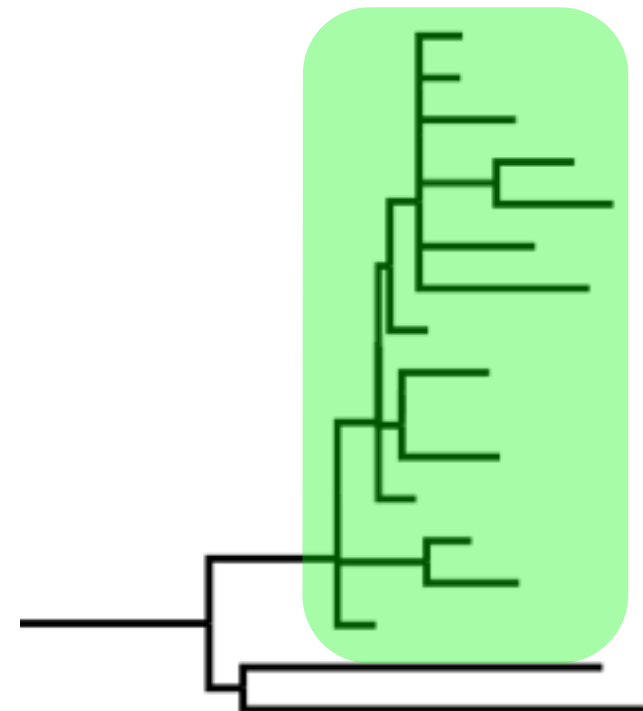
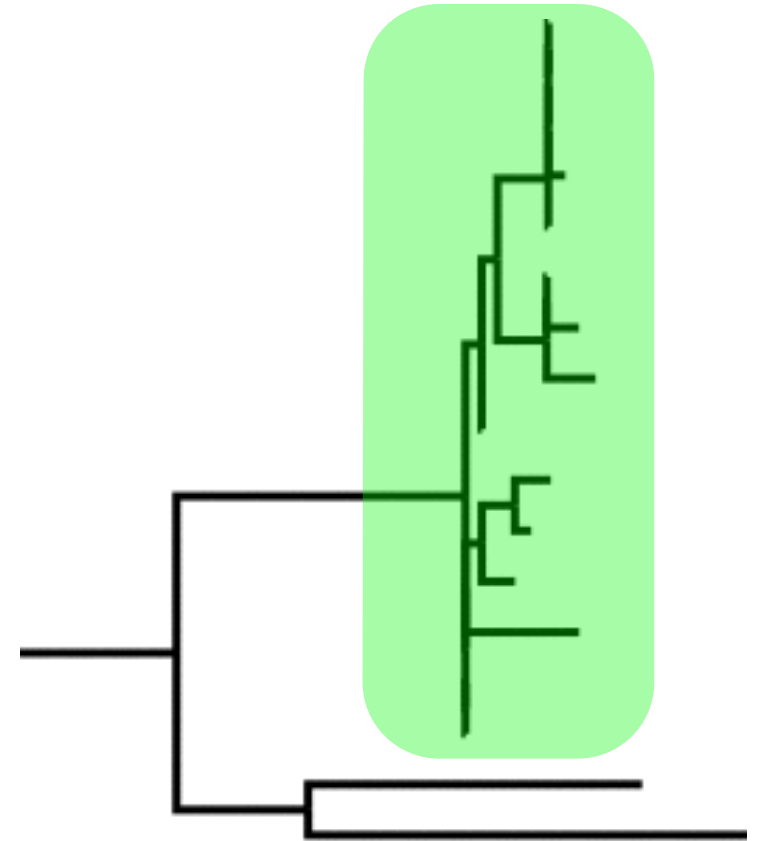
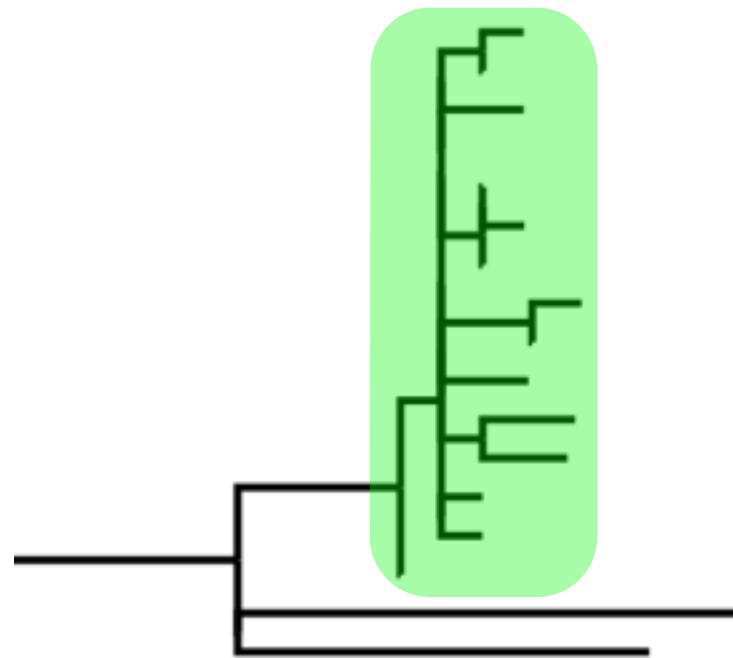
Lathraea (7)

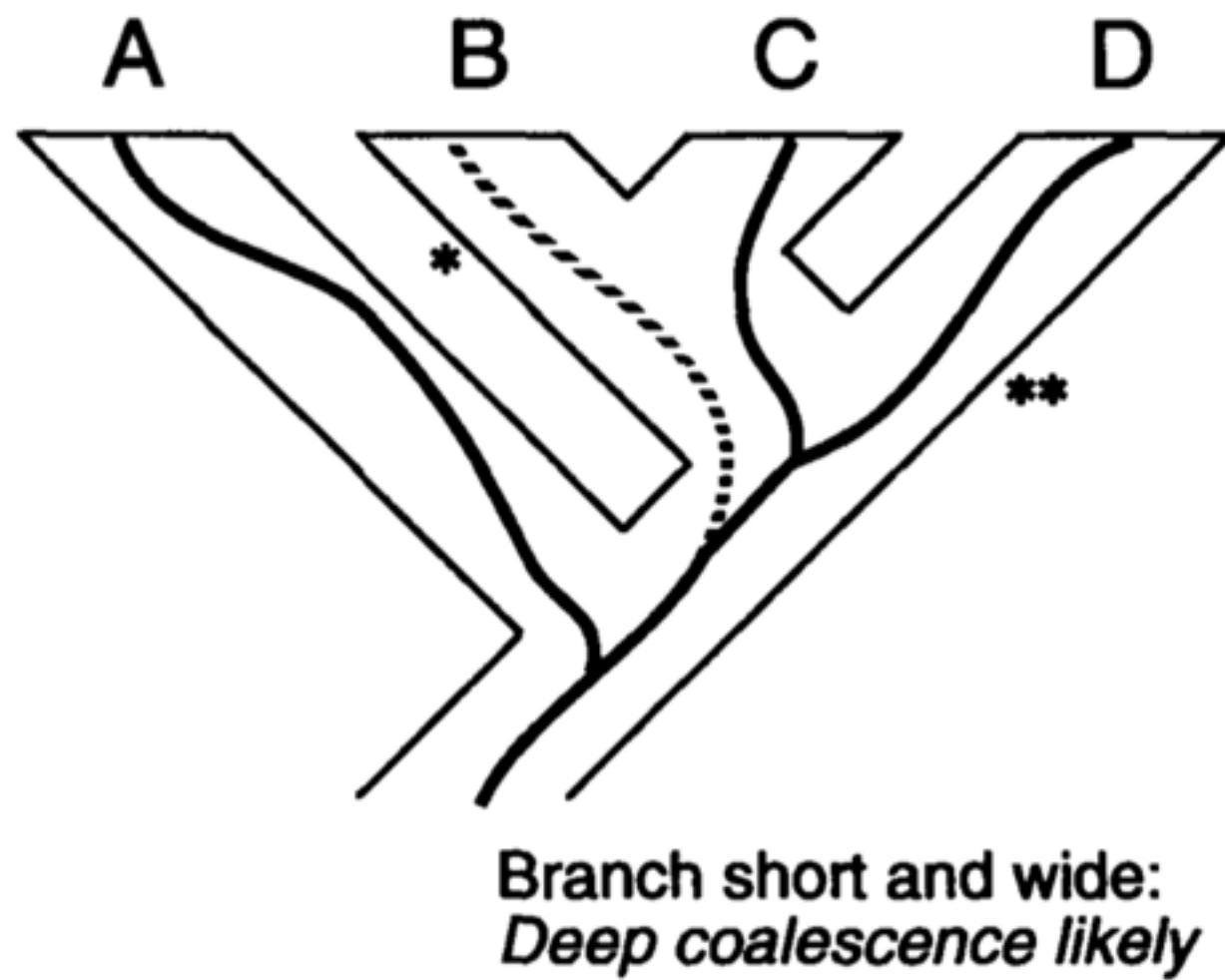
Melampyrum (35)

40.0 35.0 30.0 25.0 20.0 15.0 10.0 5.0 0.0 MA

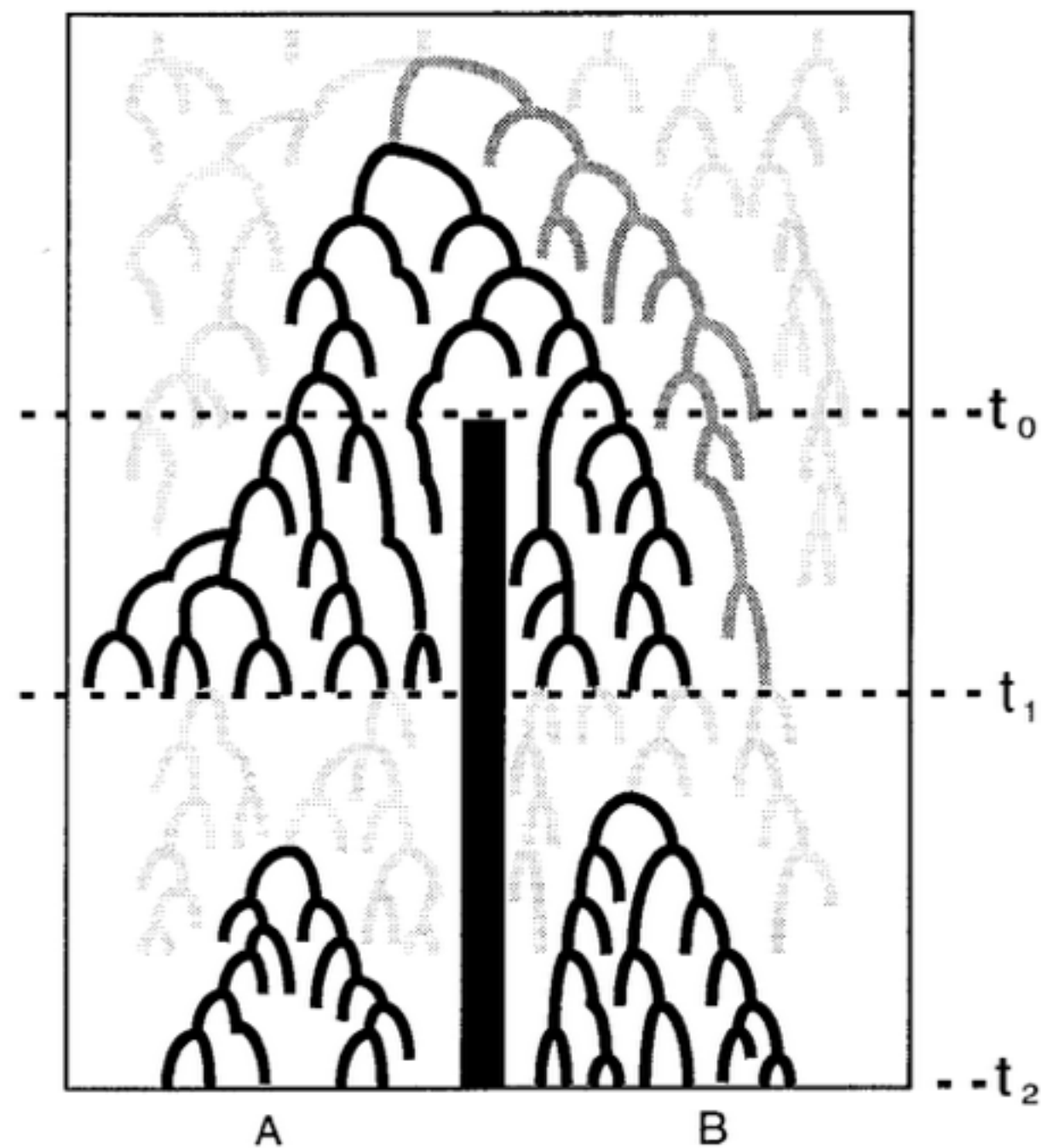


Neobartsia Uribe-Convers & Tank



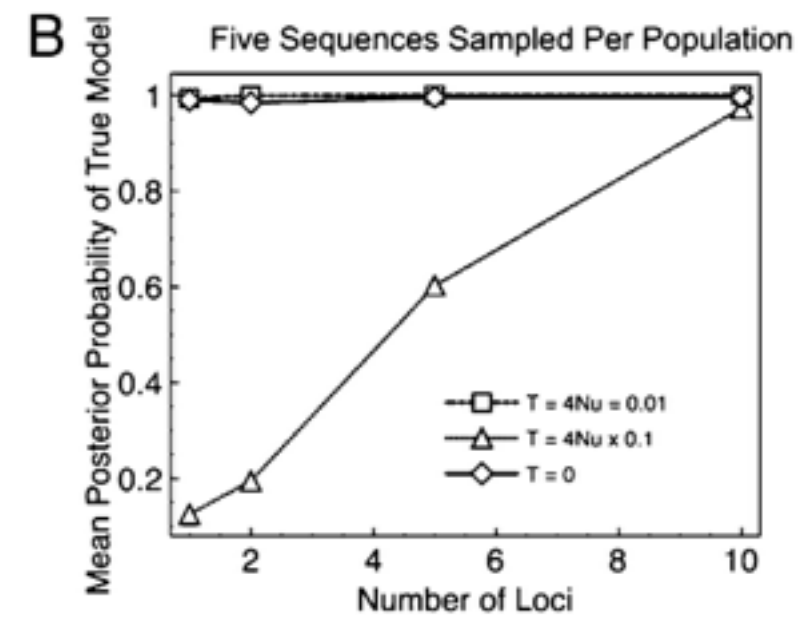
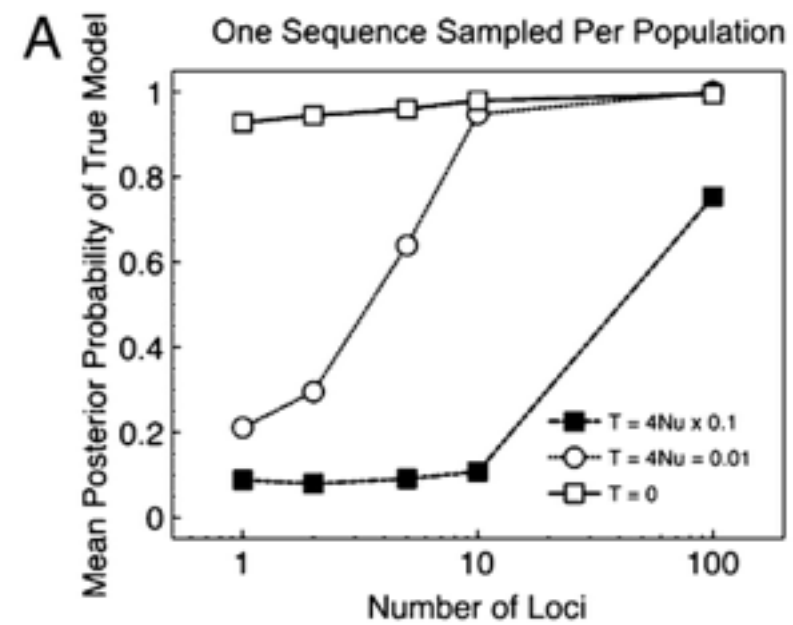
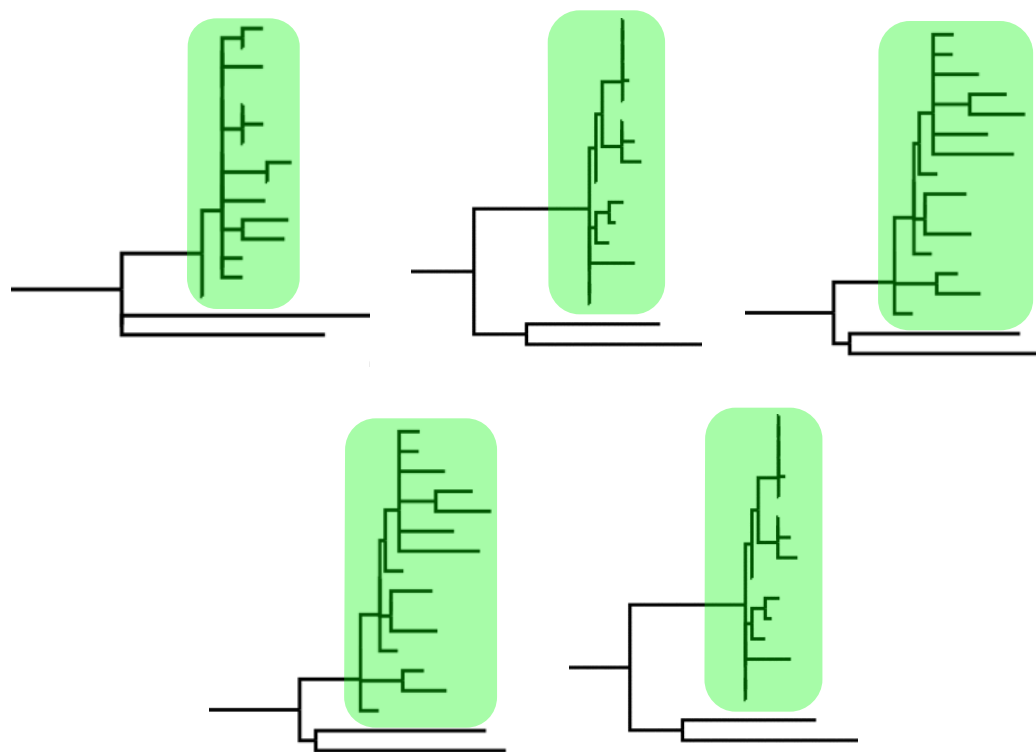


Maddison, 1997



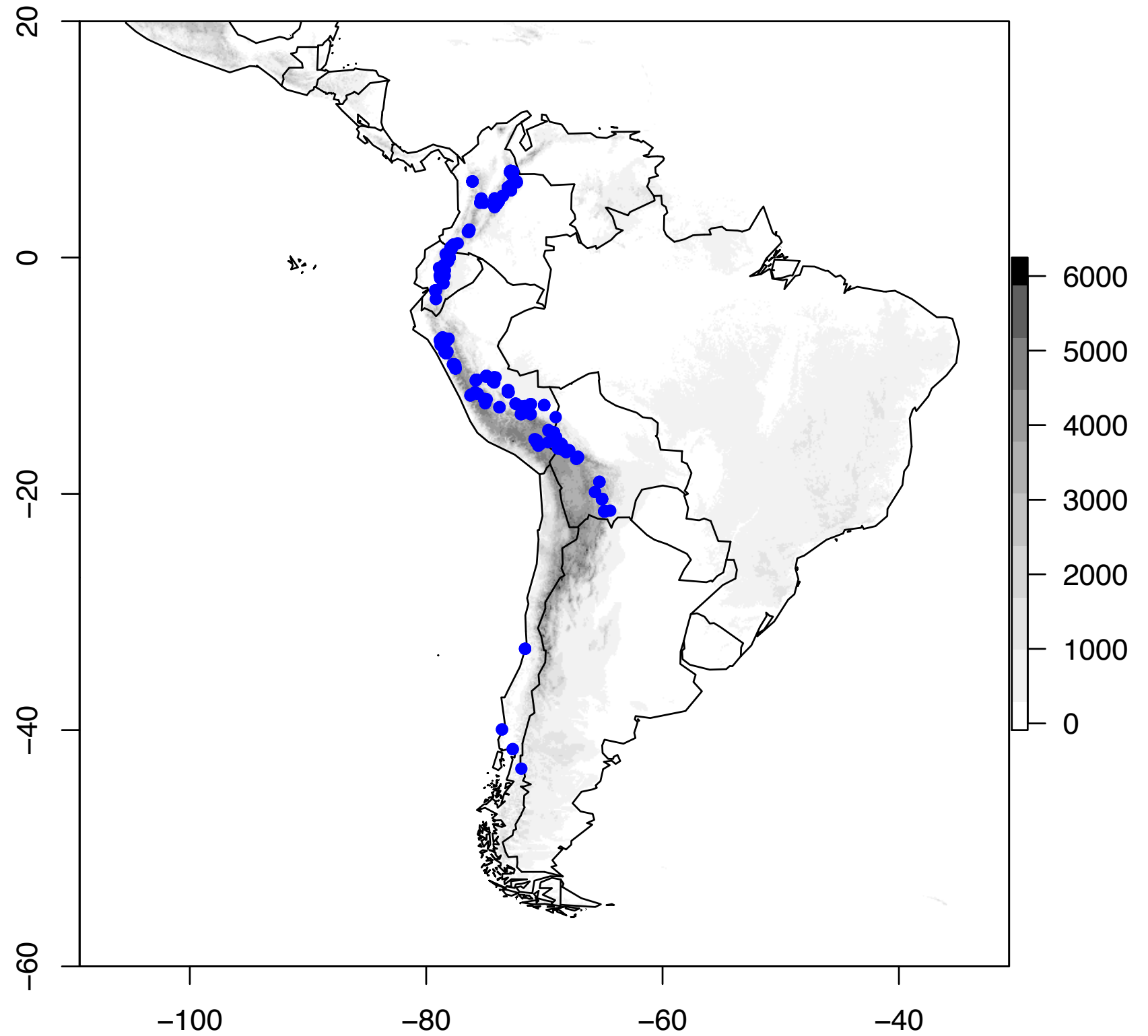
Schaal & Olsen, 2000

Multilocus dataset



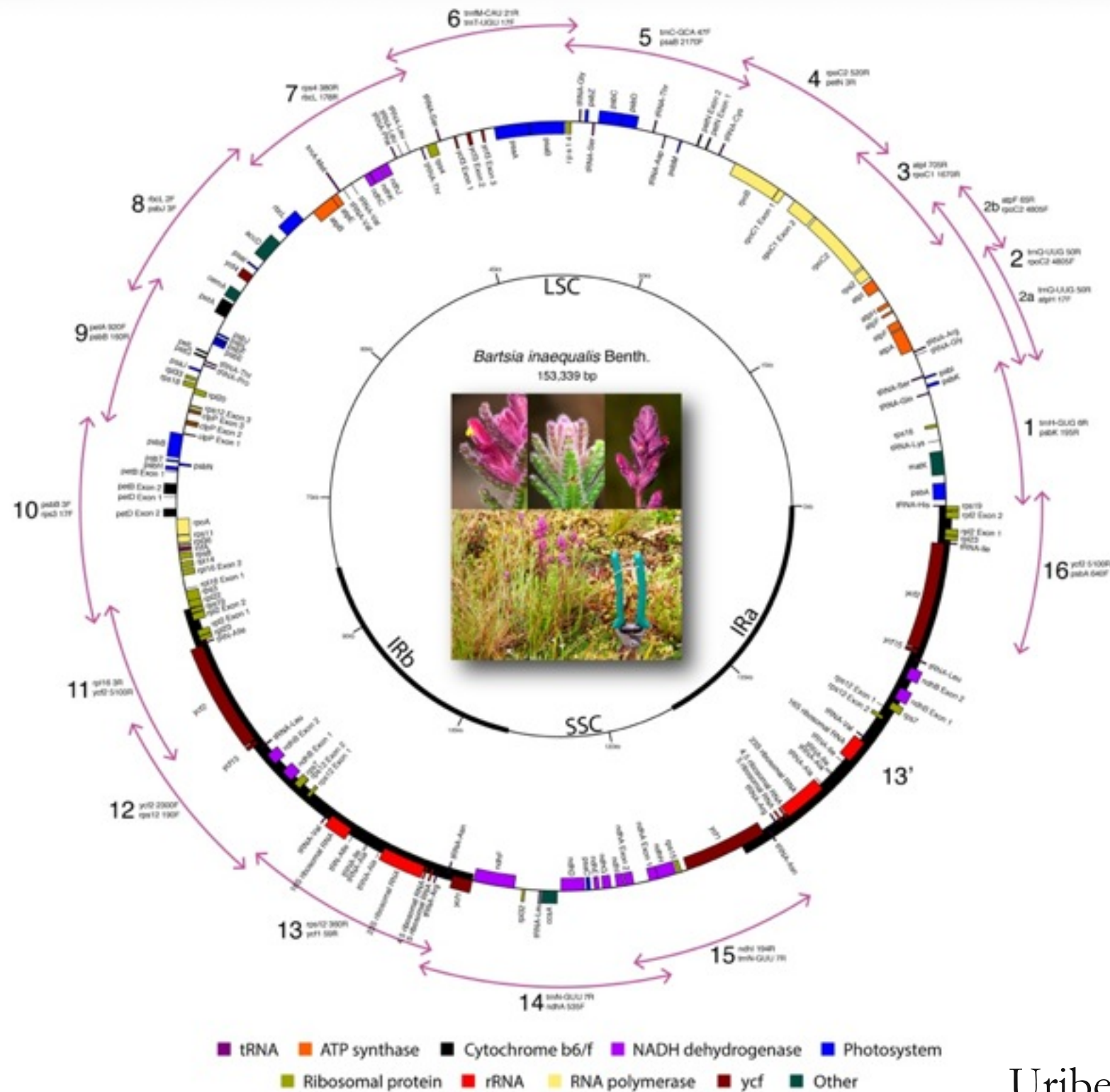
Yang & Rannala, 2010

- 505 samples *Neobartsia*
- All species
- Multiple individuals



A LONG PCR-BASED APPROACH FOR DNA ENRICHMENT PRIOR TO NEXT-GENERATION SEQUENCING FOR SYSTEMATIC STUDIES¹

SIMON URIBE-CONVERS^{2,3,5}, JUSTIN R. DUKE³, MICHAEL J. MOORE⁴, AND DAVID C. TANK^{2,3}



-48 chloroplast and 48 nuclear regions

- ca. 50,000 bp

-576 samples

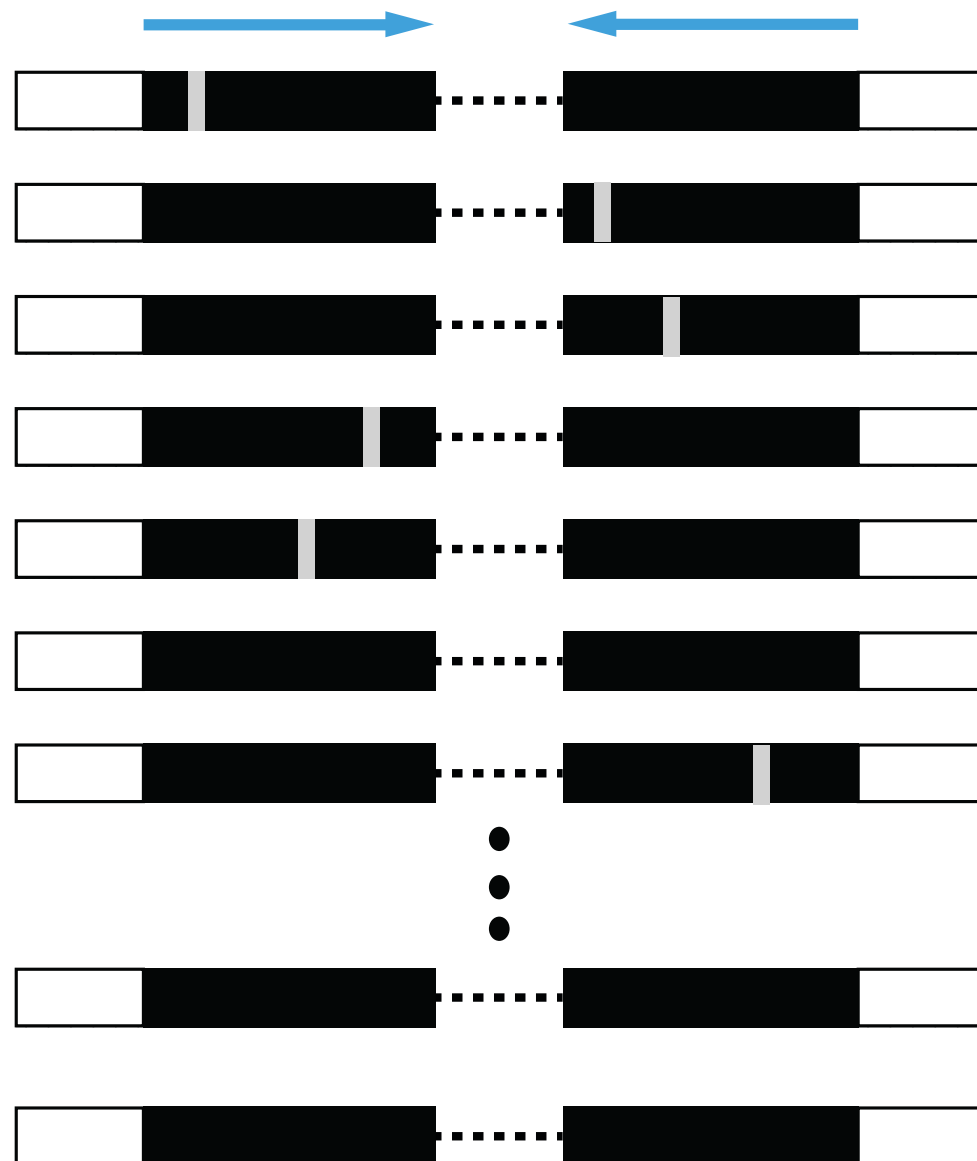
-Amplification of 24 microfluidic Fluidigm chips (**55,296 PCR**s!)

-12 for the chloroplast and 12 for the nuclear genome

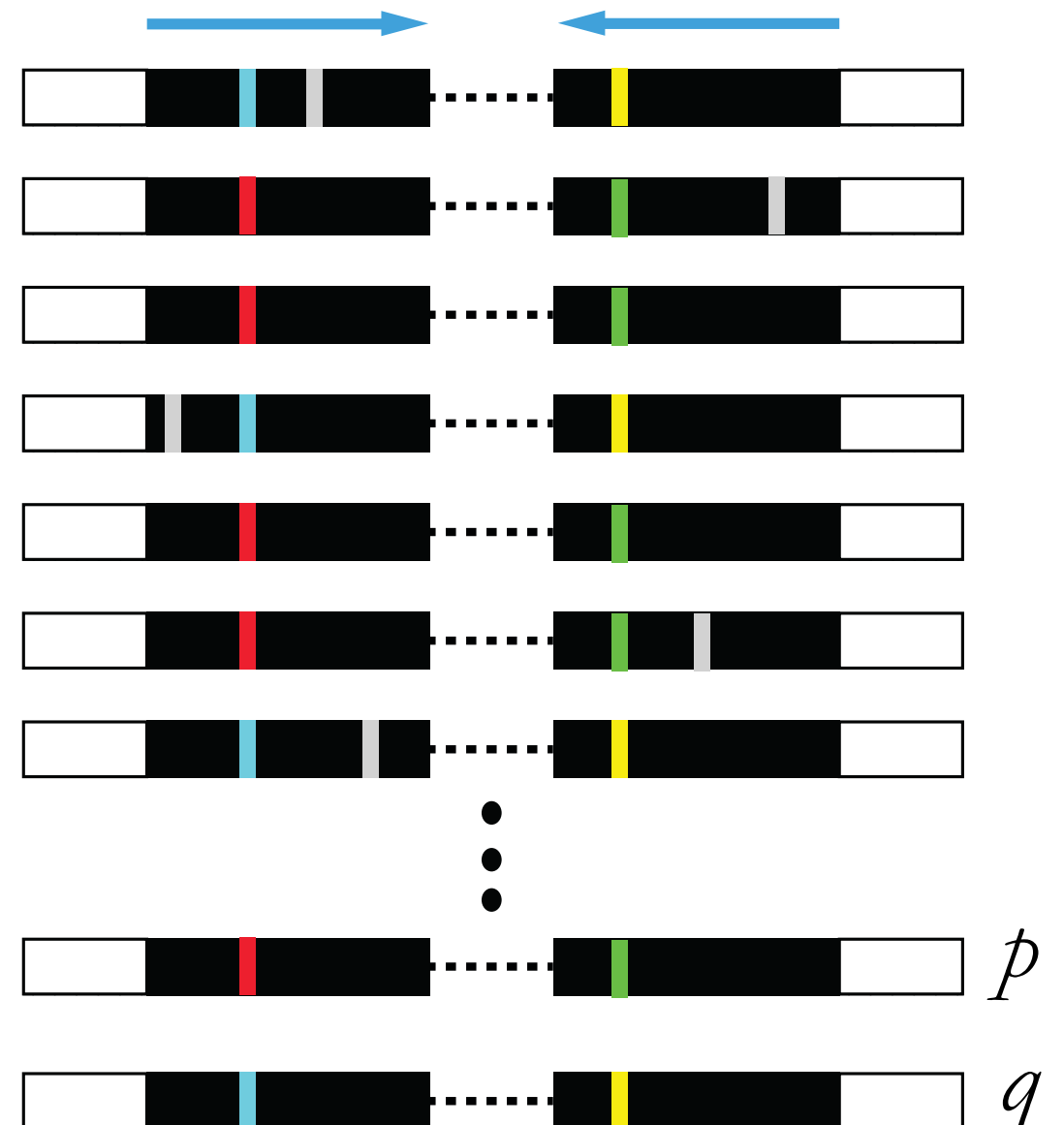
-Sequencing in Illumina MiSeq (~21 million 300 bp paired-end reads)



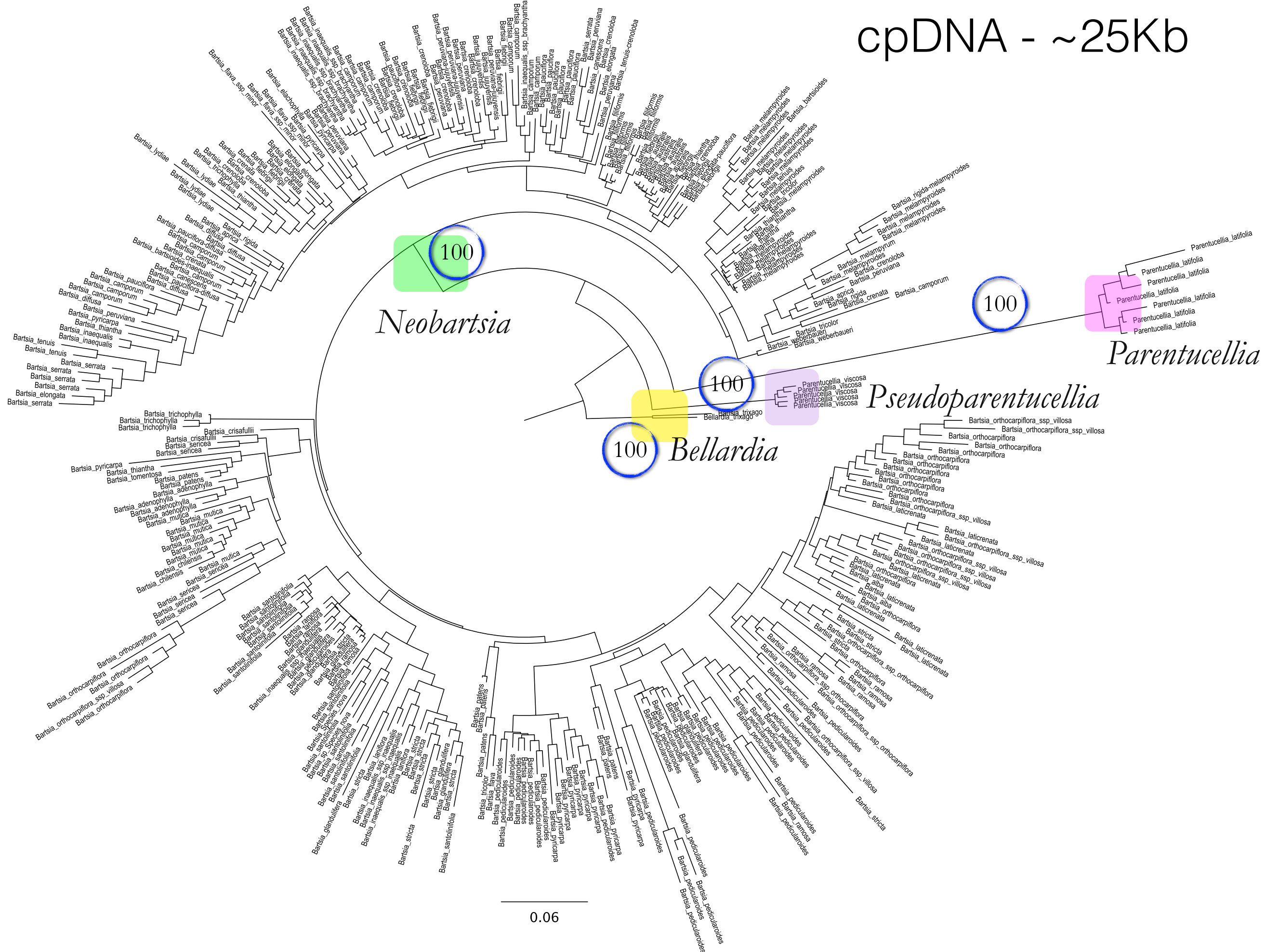
Haploid or Diploid Homozygote

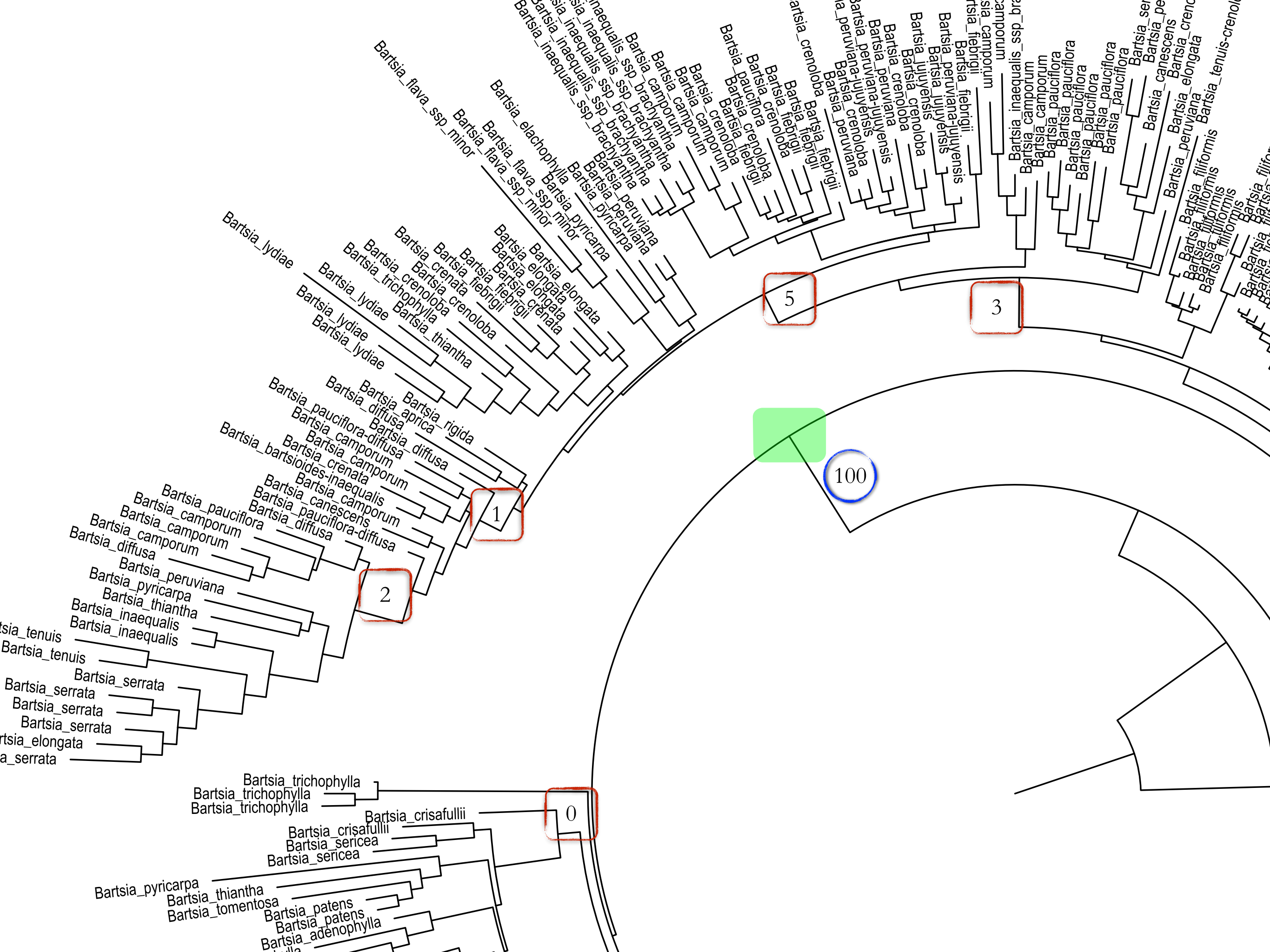


Diploid Heterozygote



cpDNA - ~25Kb

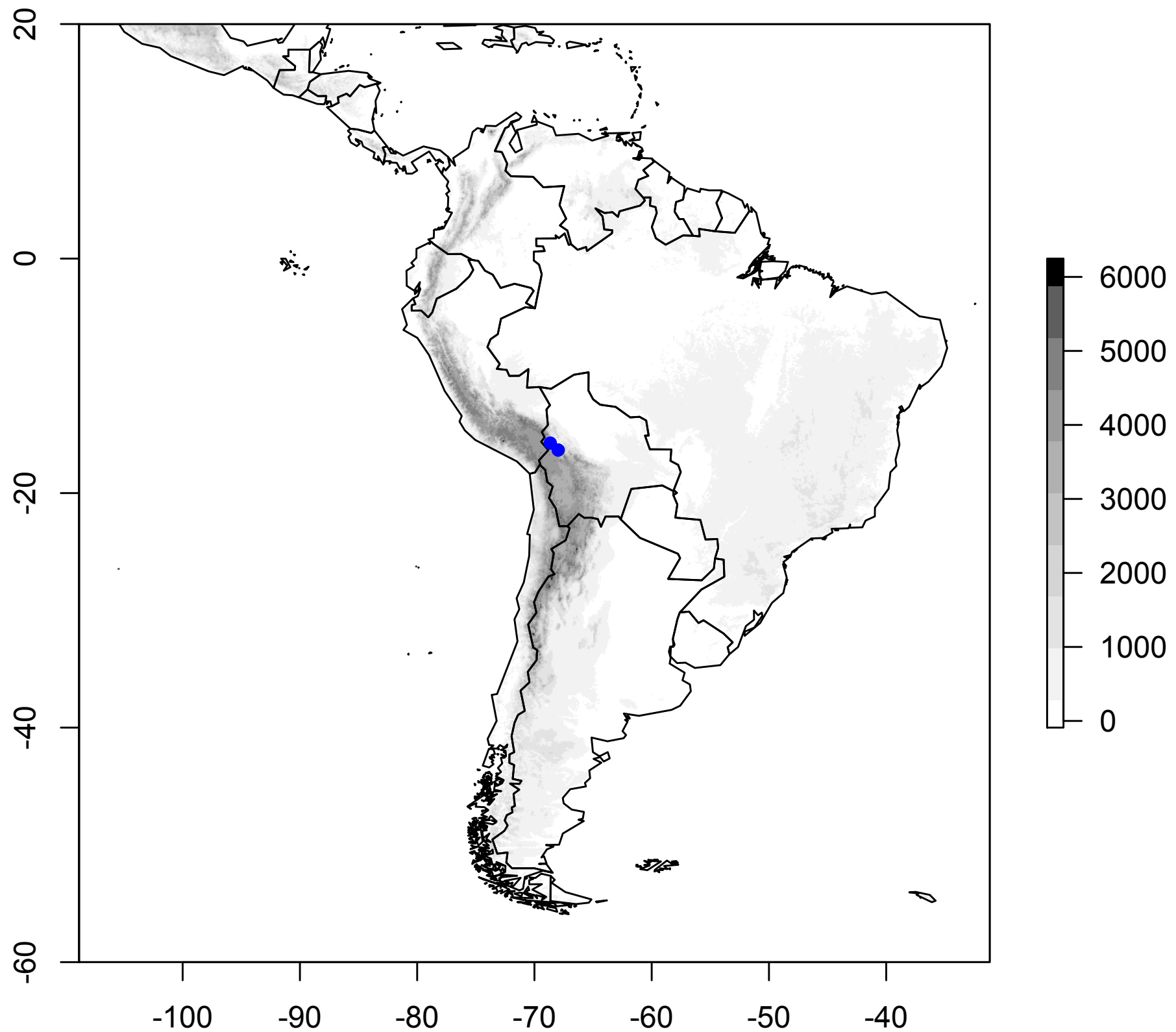




Neobartsia filiformis



Neobartsia filiformis

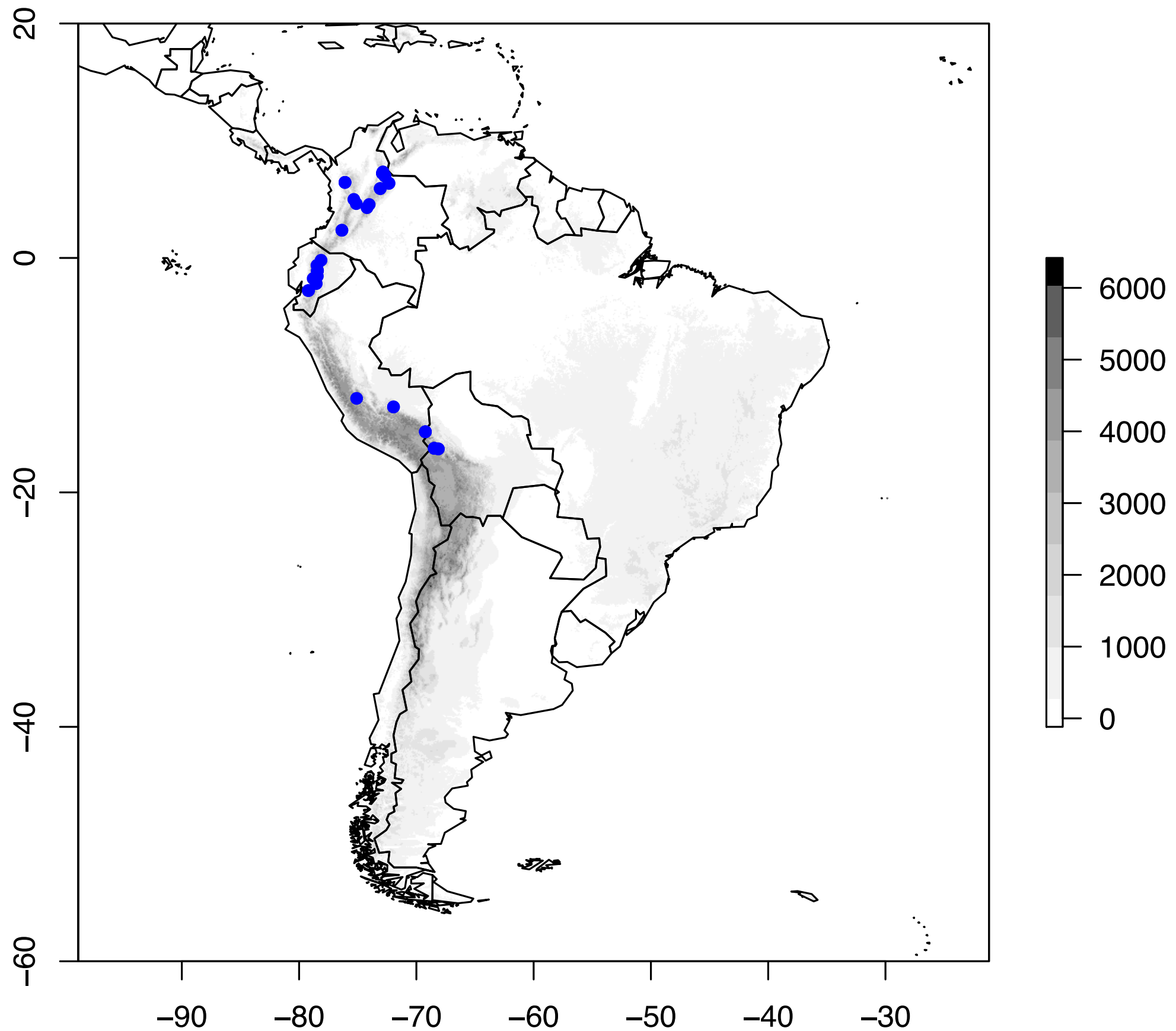


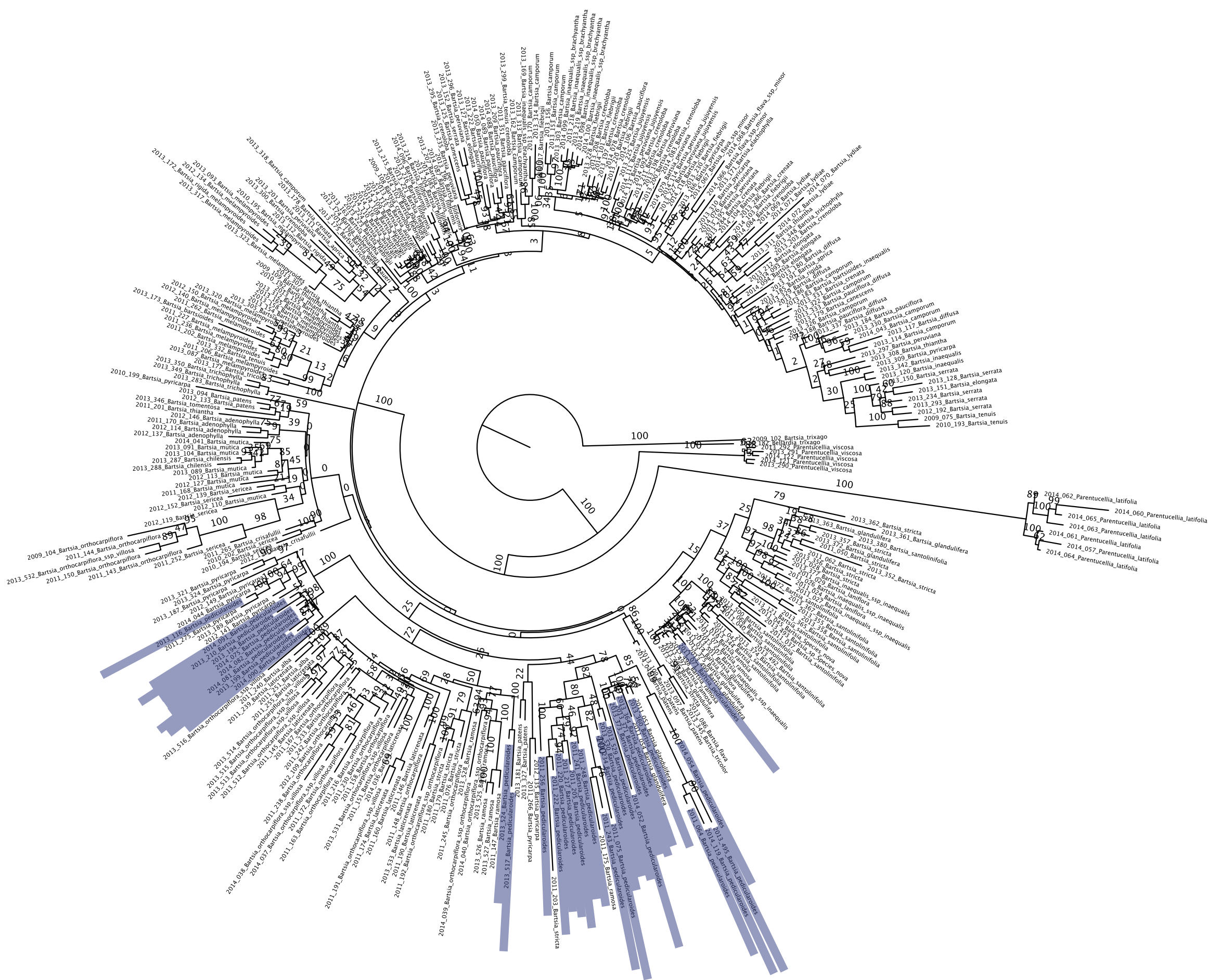


Neobartsia pedicularoides



Neobartsia pedicularoides





100

100

00040



A)

Phylogenetic tree of the 16S rRNA gene sequences of the 16 bacterial strains. The tree is rooted on the left and branches to the right. The sequences are represented by horizontal bars of varying lengths, indicating the length of the 16S rRNA gene. The tree shows a clear separation between the two groups of strains, with one group forming a distinct cluster and the other group forming a separate cluster. A scale bar at the bottom indicates a distance of 0.05 substitutions per site.

B)

0.00

Coalescent-based methods **with allelic** information

***BEAST**

Bayesian Inference of Species Trees from Multilocus Data

Joseph Heled^{*,1} and Alexei J. Drummond^{1,2,3}

¹Department of Computer Science, University of Auckland, New Zealand

²Bioinformatics Institute, University of Auckland, New Zealand

³Allan Wilson Centre for Molecular Ecology and Evolution, University of Auckland, New Zealand

MP-EST

A maximum pseudo-likelihood approach for estimating species trees under the coalescent model

Liang Liu^{1*}, Lili Yu², Scott V Edwards³

Coalescent-based methods **with allelic** information

***BEAST**

37.8 hours (~ 1.5 days) per million generation

MP-EST

Not possible to run, exceeds memory

Coalescent-based methods **with allelic** information

Reduced dataset - 3 individuals per species

***BEAST**

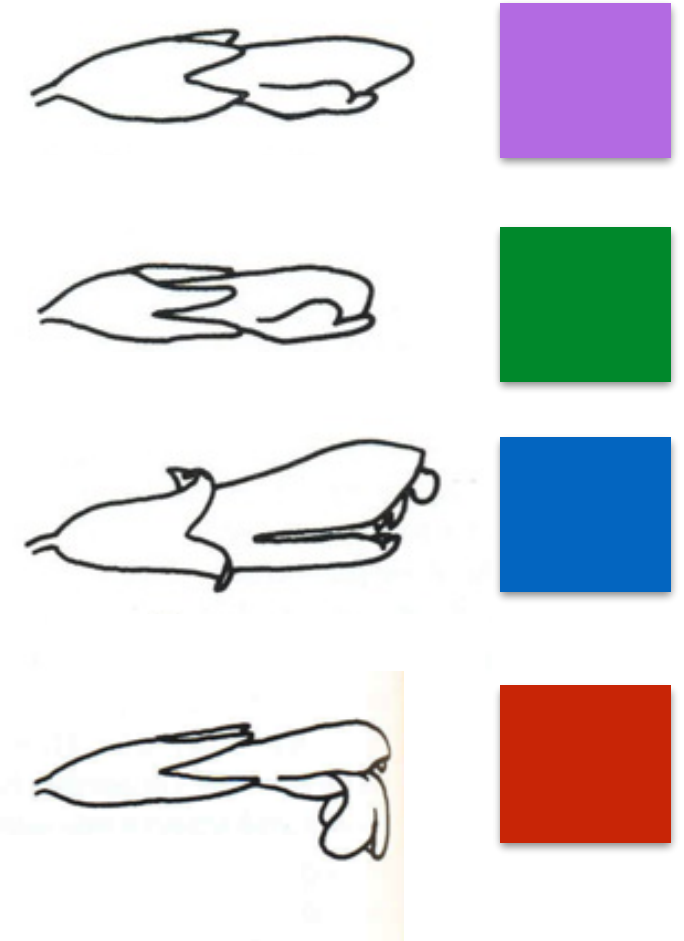
3.5 hours per million generation

MP-EST

ca. one month to finish

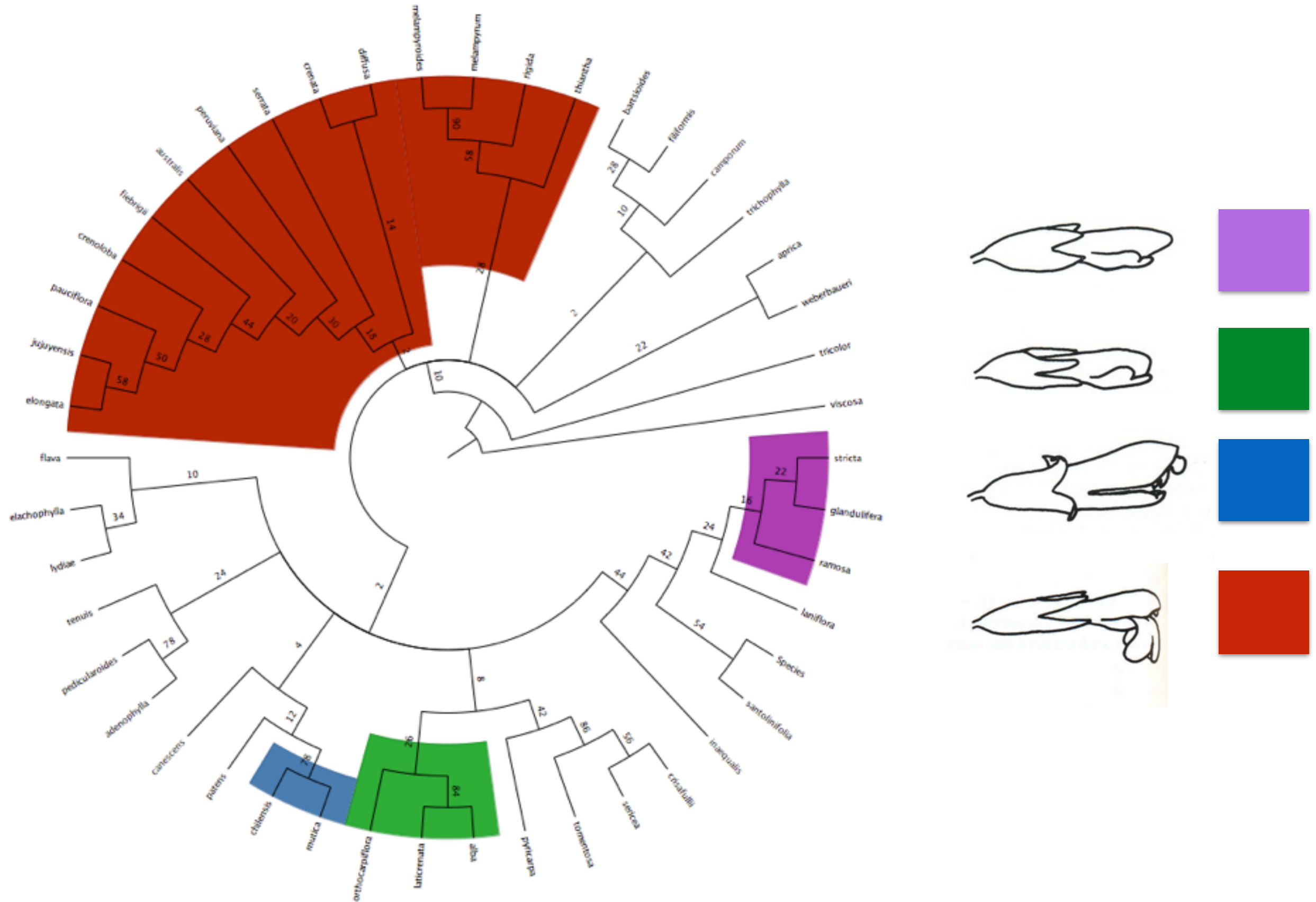
Data **without** allelic information, ambiguity code instead

Species tree estimation - STAR

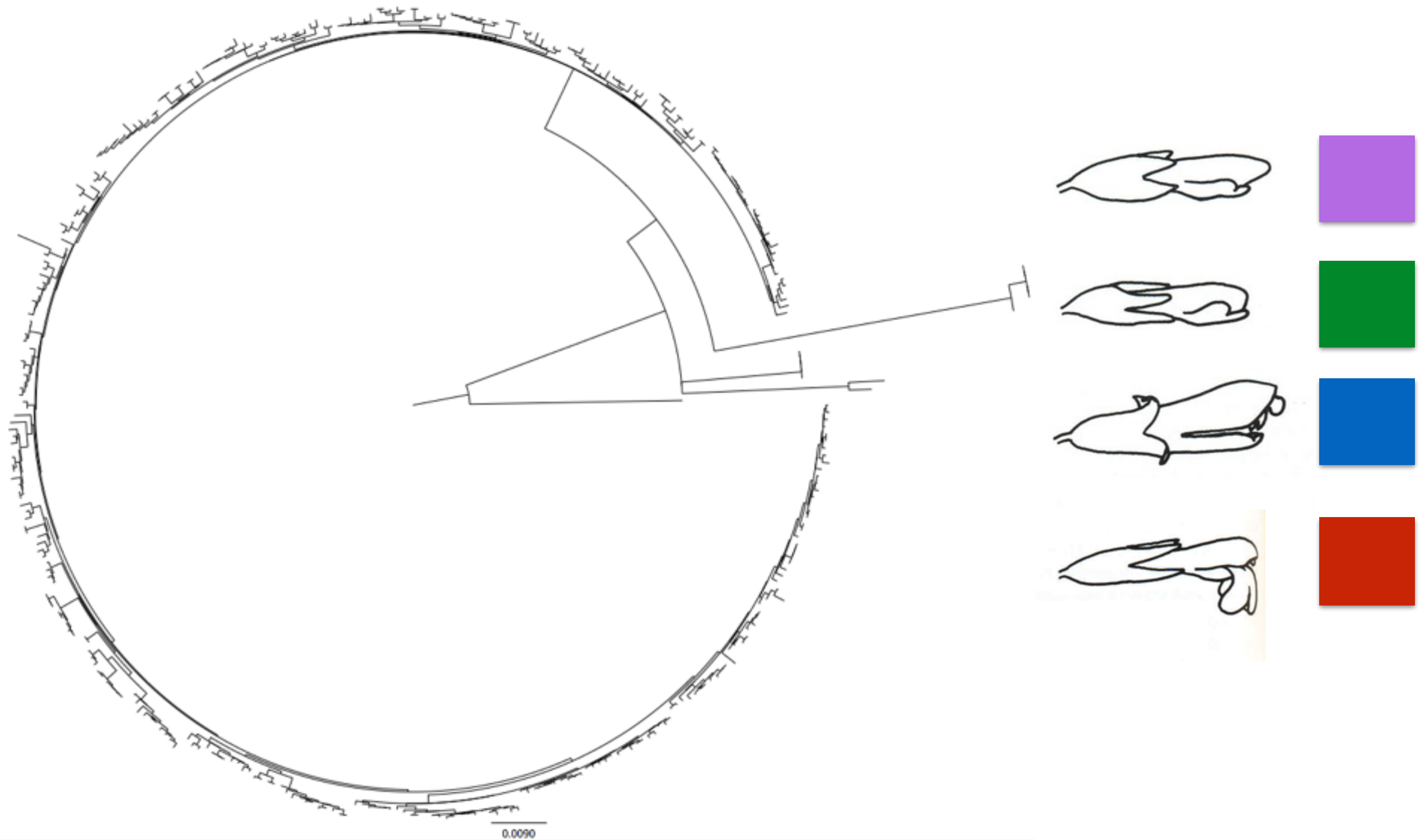


Data **without** allelic information, ambiguity code instead

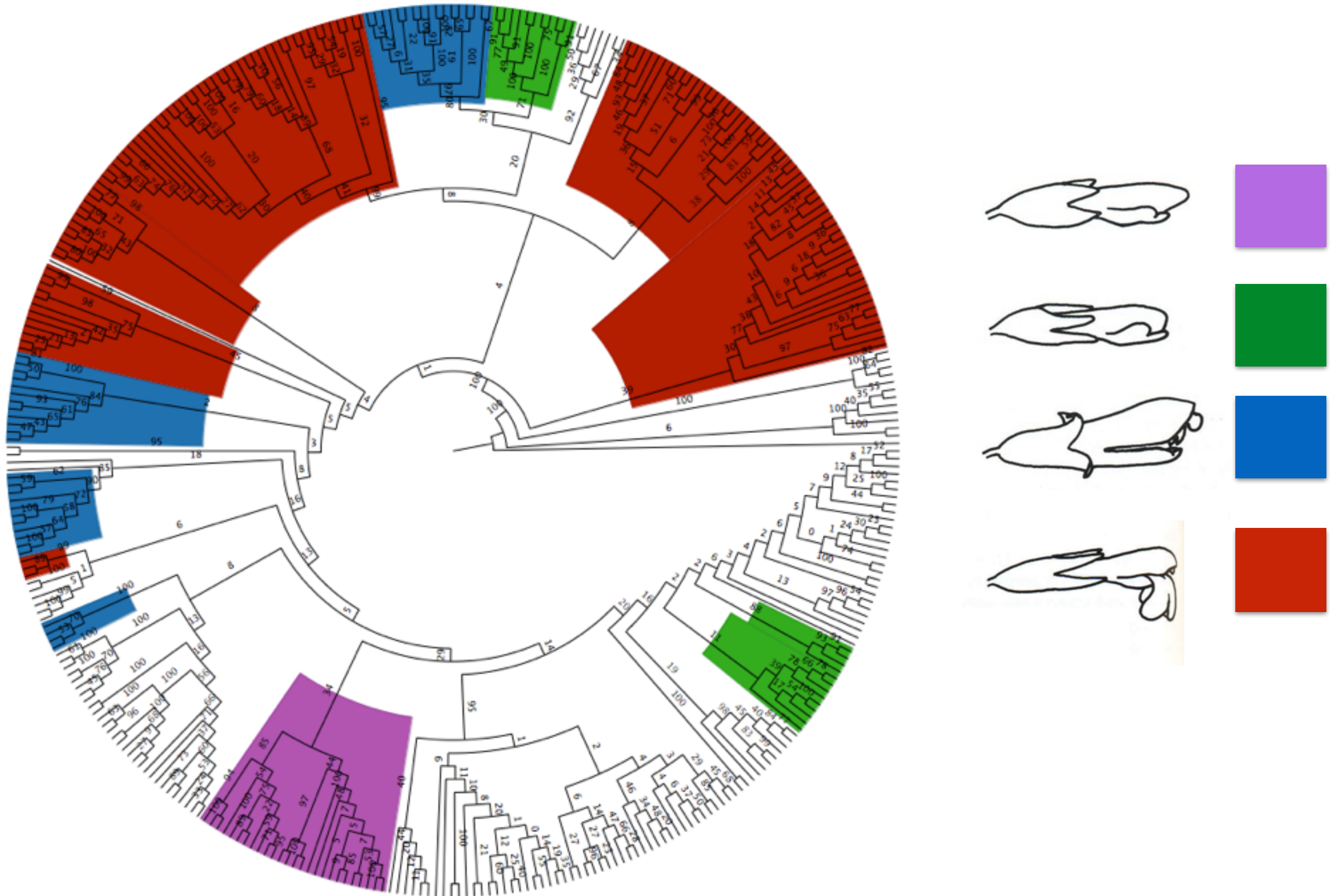
Species tree estimation - STAR



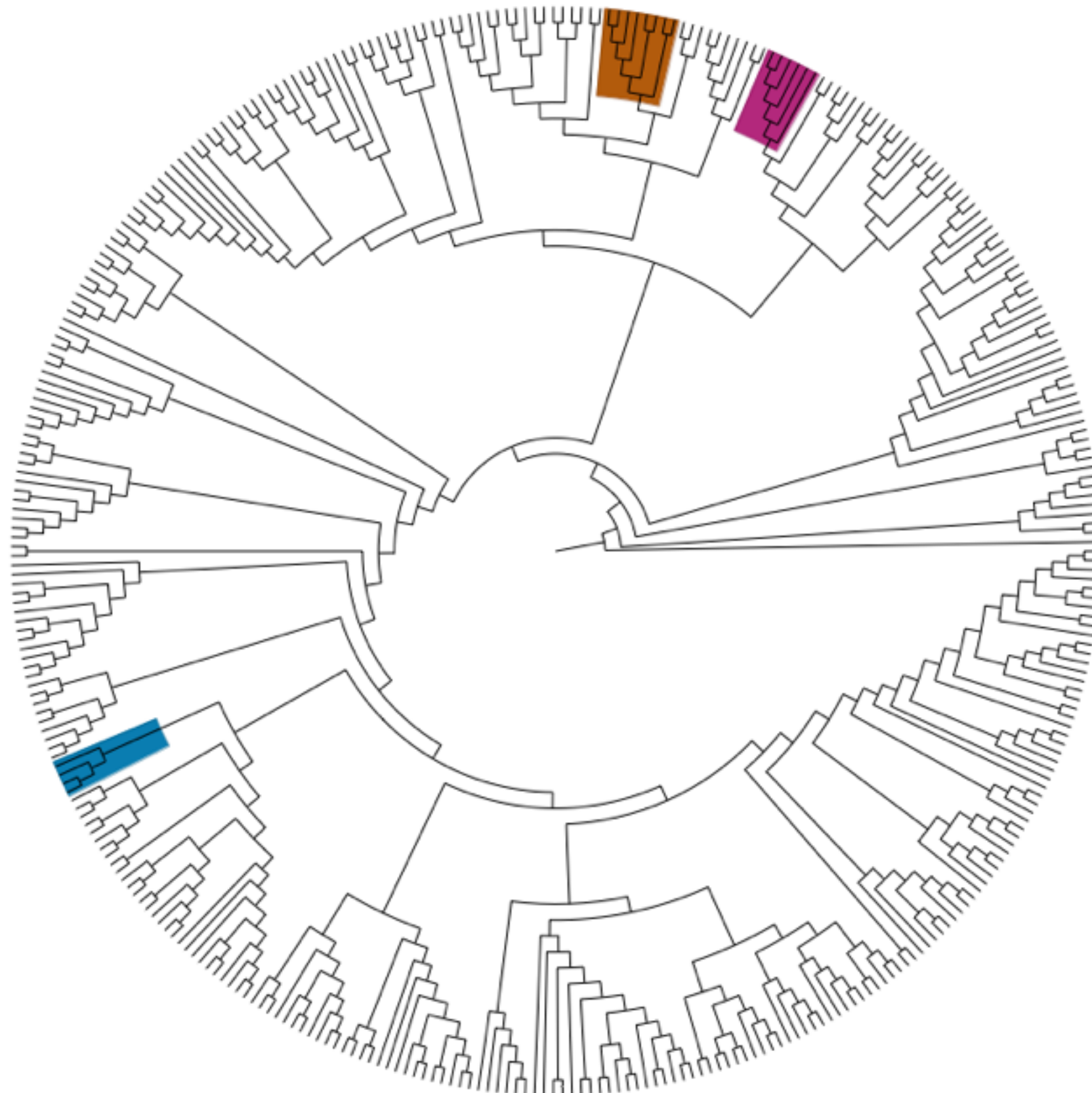
Data **without** allelic information, ambiguity code instead
Traditional methods - Concatenated analysis
of cpDNA and nuclear loci ~50kb



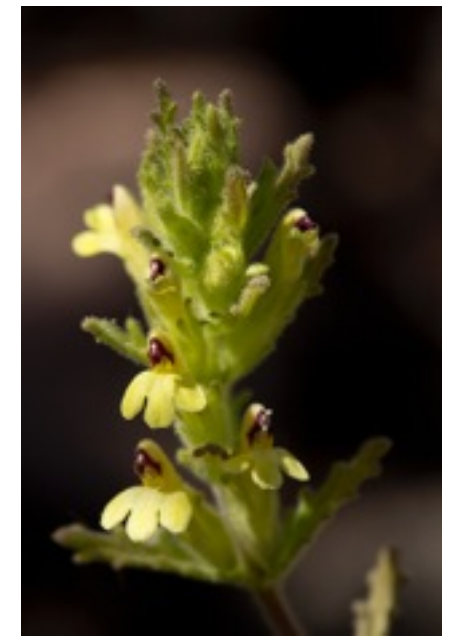
Data **without** allelic information, ambiguity code instead
Traditional methods - Concatenated analysis
of cpDNA and nuclear loci ~50kb



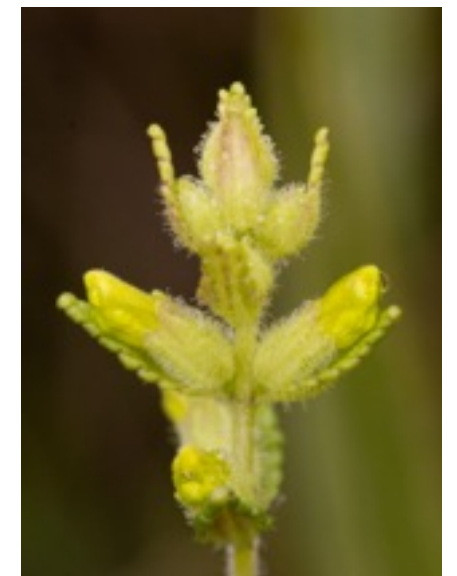
Data **without** allelic information, ambiguity code instead
Traditional methods - Concatenated analysis
of cpDNA and nuclear loci ~50kb



N. serrata

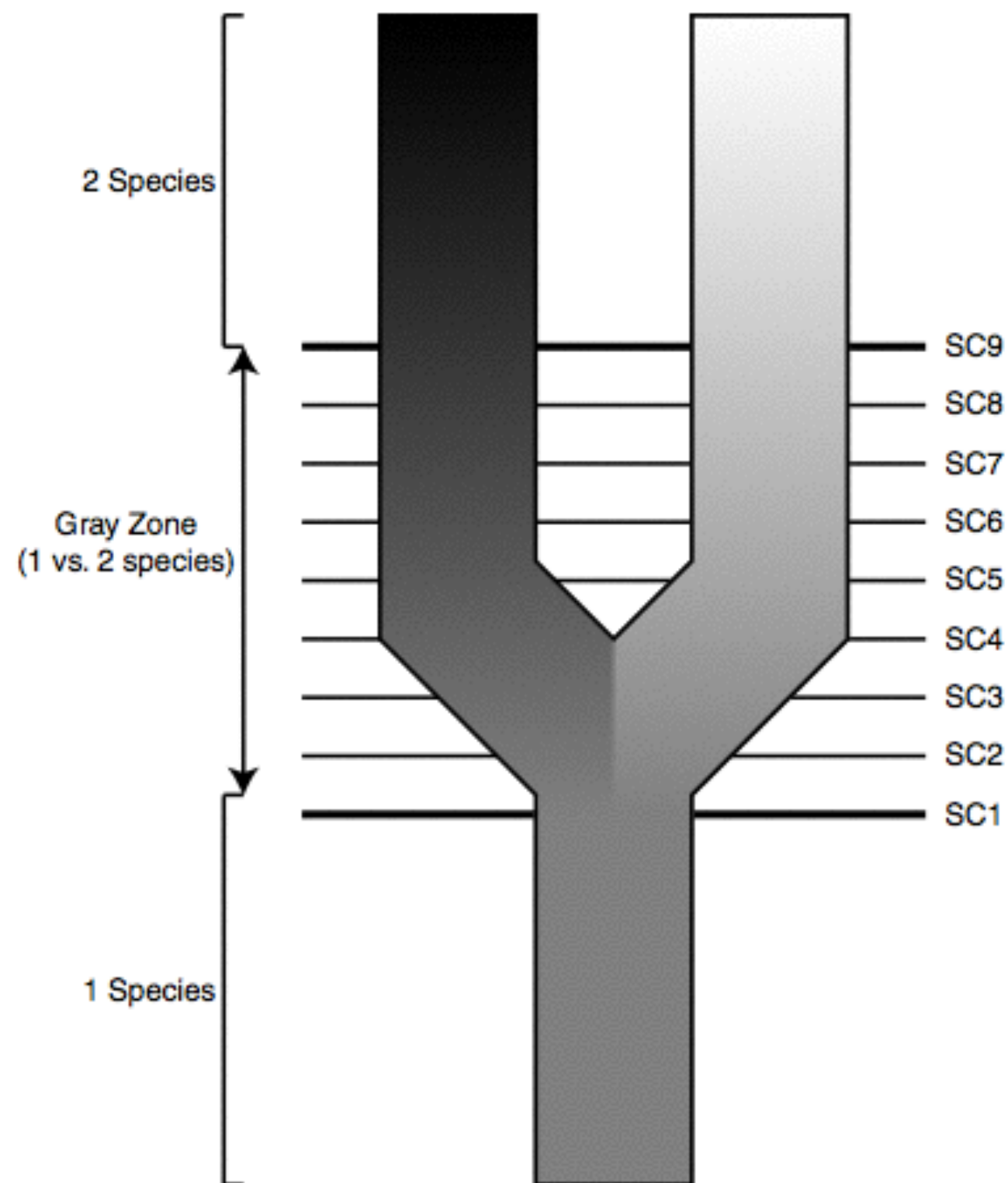


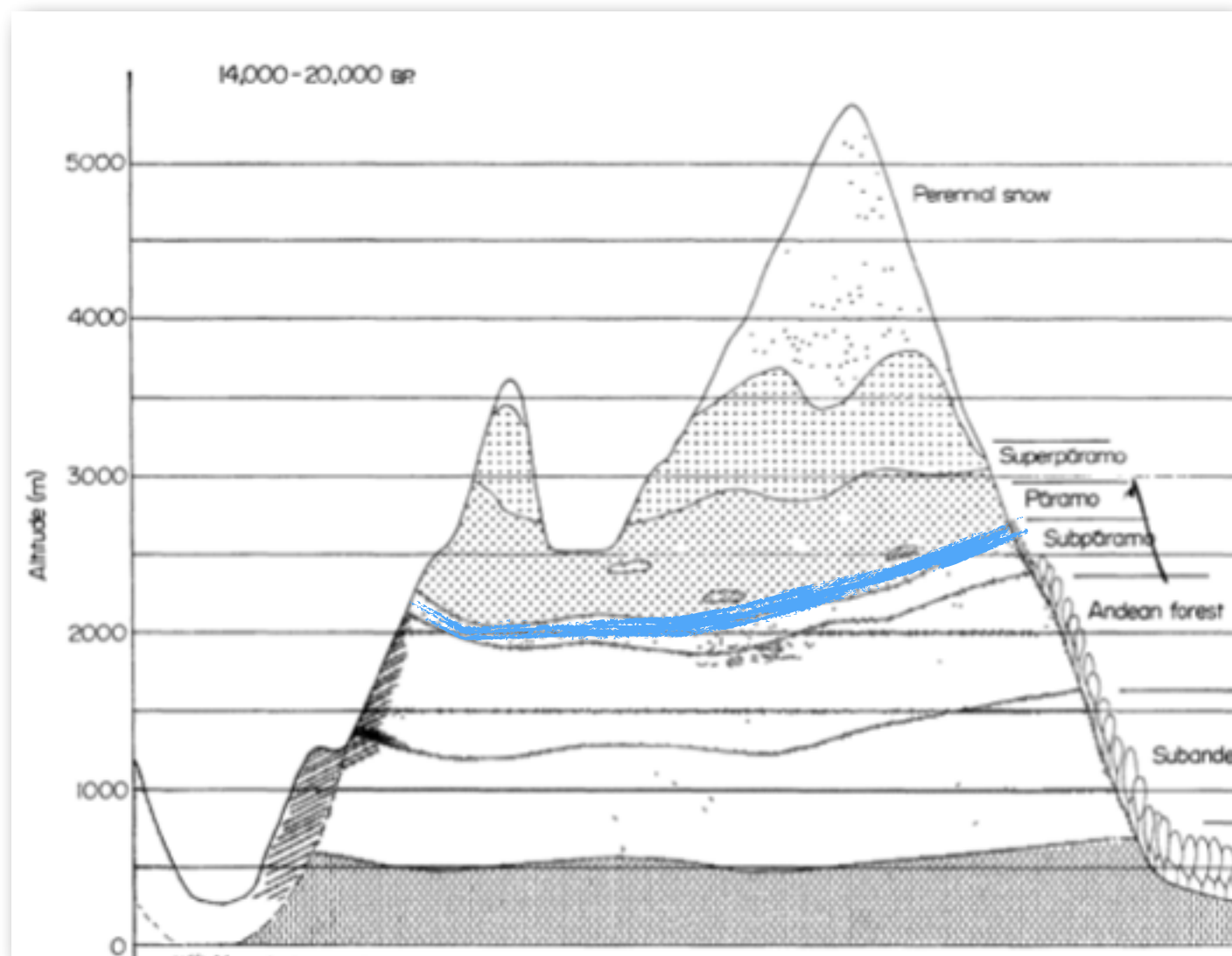
N. filiformis



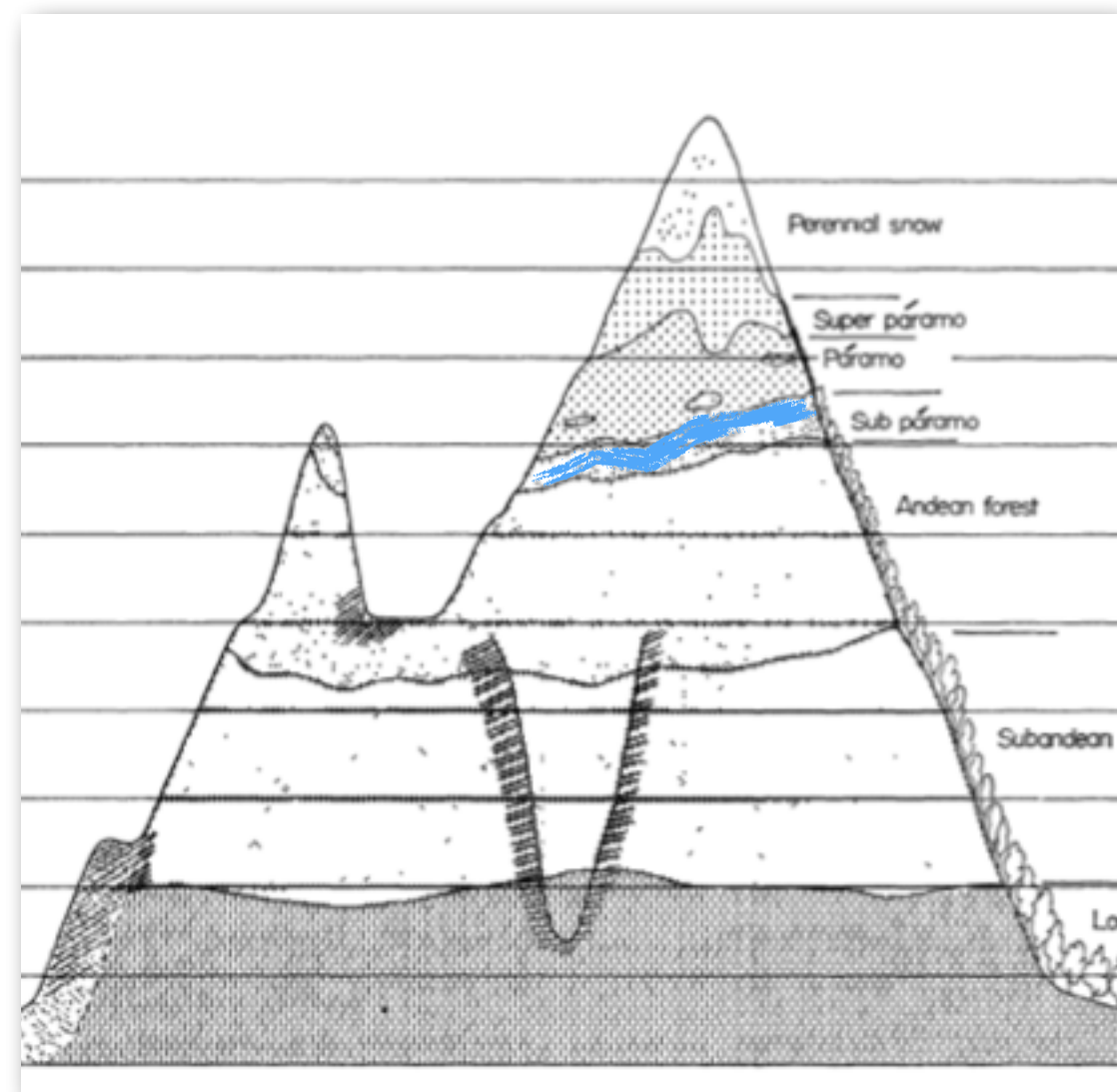
N. adenophylla







20,000 BP



Present

#nextgenerationproblems



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Acknowledgments

Tank lab

Diego Morales-Briones, Hannah Marx
Sarah Jacobs, Maribeth Latvis

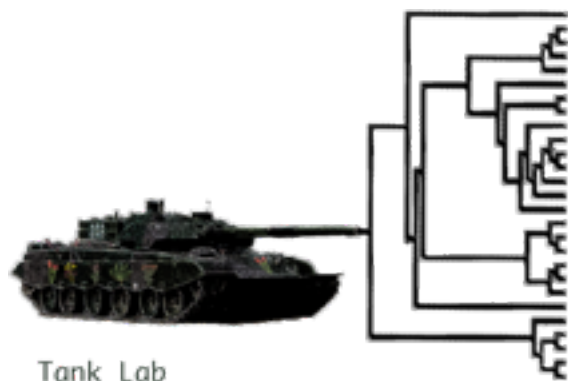
Olmstead lab

Dick Olmstead, John Chau, Laura Frost

Nicolai Nürk

Laura Kubatko

Segundo Leyva, Mario Zapata



Tank Lab
FIGHTING POLYTOMY SINCE 2008

